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Subject:

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Searcher:
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TYPE OF SEARCH:	
NA Sequences:	
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VENDOR/COST (w	here applic.)
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Q27238 anopheles g
P31692 chlorella k
P18238 saccharomyc
P27080 chlamydomon
Q09188 schizosacch
Q09188 schizosacch
Q2234 gossypium h
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RC TISSUE-Liver; RX MEDLINE=88124845; PubMed=2829183; RA Houldsworth J., Attardi G.; RT "Two distinct genes for ADP/ATP translocase are expressed at	human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [4] CENTRACE OF 16.288 EDDM N.A.	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smai Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000	Richards S., Worley K.C., Hale S., Garcia A.M., Gay Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., G Fahey J., Helton E., Ketteman M., Madan A., Rodrigu Whiting M., Madan A., Young A.C., Shevchenko Y., Bo Blakesley R.W., Touchman J.W., Green E.D., Dickson i	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J Diatchenko L., Marusina K., Farmer A.A., Rubin G.M. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci Raha S.S., Loquellano N.A., Peters G.J., Abramson R Rosak S.A. McRean D.T. McKernan K.T. Malek T.A.	ye, and Lung; ed=12477932; ld E.A., Grouse L.H., Derge J.G. F.S., Wagner L., Schanfer C.K., i	"DAM sequences of two expressed nuclear genes for ADP/ATP translocase."; I. Wol. Biol. 206:261-280(1989). [2] SEQUENCE FROM N.A. Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bou Margolin J.F.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ data	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata Mammalia; Eutheria; Primates; Catarrhini; Hominida NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=89236396; PubMed=2541251; Cozens A.L., Runswick M.J., Walker J.E.;	TANDARD; PRT; 298 AA. 12, Created) 16, Last sequence update) 42, Last annotation update) protein, liver isoform T2 (ADP/ATP ide translocator 3) (ANT 3).
xpressed at the mRNA	•	M., Smailus D.E., , , 000 full-length	ay L.J., Hulyk S.W., Gibbs R.A., gues S., Sanchez A., Bouffard G.G., n M.C.,	M., Hong L., T.L., Scheetz T.E., ci P., Prange C., ci P., Prange C., R.D., Mullahy S.J., Ginaratha P H		numan mitochondrial uck J., Gibbs R.A., abases.	a; Euteleostomi; ae; Homo.	P translocase 3)

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TRANSMEM 12
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FUNCTION: CATALYZES THE EXCHANGE OF ADP
MITOCHONDRIAL INUBR MEMBRANE.
SUBUNIT: Homodiner.
SUBCELLULAR LOCATION: Integral membrane
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drion; Inner membrane; Repeat; Transmembrane;
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S THE EXCHANGE OF ADP AND ATP ACROSS
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PROSITE; P800215; MITOCH_CARRIER;
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Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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                                                                                                   SEQUENCE
                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                         PIR; B43646; B43646; Mit_carrier. InterPro; IPR002067; Mit_uncoupling. InterPro; IPR002030; Mit_uncoupling. InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                            EMBL; M24103; AAA30769.1; -.
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P32007;
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                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                Multigene
                                                                                                                                                                                                                                               Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89229093; PubMed=2540808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inner membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                 291;
                                                              Similarity
             MTEQA1SFAKDFLAGG1AAAISKTAVAPIERVKLLLQVQHASKQ1AADKQYKGIVDCIVR
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 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                  Conservative
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                                                              98.0%;
97.7%;
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3) (ANT 3).
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                                               Score 1512; D
Pred. No. 1.9e
4; Mismatches
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                                               e 1512; us .,
No. 1.9e-125;
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ADP/ATP translocase
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                                                                                                                                                                                                                                            Transmembrane;
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                                                                          Length
                                                   Indels
                                                                             298;
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ADT2 HUMAN
P05141; O43350;
13-AUG-1987 (Rel
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J. Biol.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
Mazzarella R.A., Schlessinger D., Chen E.Y.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          growth-regulated.";
J. Biol. Chem. 262:4355-4358(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The
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MEDLINE=90375457; PubMed=2168878;
Chen S.-T., Chang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-PSB-2003 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADP/ATP (Adenine nucleotide translocator 2) (ANT 2).
SLC25A5 OR ANT2.
                                                                        "Two distinct genes for ADP/ATP translocase are level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                        MEDLINE=88124845; PubMed=2829183;
                                                                                                                                                                       rissum=Liver;
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                         SEQUENCE FROM N.A.
Becker M., Graves T.,
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of a cDNA for a growth-regulated.";
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87166056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                              D.-H., Kagan J., Chen S.-T., Chang C.-
he human fibroblast adenine nucleotide
oning and sequence.",
Biol. Chem. 265:16060-16063(1990).
            DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier
                                                  SUBCELLULAR LOCATION: Integral
                                                              SUBUNIT: Homodimer.
                                     inner membrane
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e translocator gene. Molecular
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InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mitocarr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion; Inner membrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0015207; F:adenine transporter activity; TAS. GO; GO:0006832; P:small molecule transport; TAS.
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                                                                                                    QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK
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ADT2 RAT Q09073; 01-FEB-1995

(Rel. 31, Created)

STANDARD;

PRT;

298 A

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Query Match
Best Local (
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TRANSMEM 12
TRANSMEM 73
TRANSMEM 17
TRANSMEM 176
TRANSMEM 176
TRANSMEM 214
TRANSMEM 273
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-i-FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBERNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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InterPro; IPR002030; Mit_uncoupling
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Last 16-OCT-2001 (Rel. 40, Last ADP, ATP carrier protein, f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D12771; BAA02238.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Liver; MEDLINE=94002161; PubMed=8399300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLC25A5 OR ANT2
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the mitochondrial carrier family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM
                                                               GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                             I PKEQGVLSFWRGNLANVI RYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                               MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                      MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                        GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFKGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                        IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
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91.9%;
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fibroblast isoform (ADP/ATP
slocator 2) (ANT 2).
                                                                                                                                                                                                                                                                                      15;
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Pred. No. 4.3e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence update)
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                                                                                                                                                                                                                                                                                                                                                                       6A59204B987EFE35 CRC64;
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; Murinae; Rattus.
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P51881; Q61311;
01-OCT-1996 (Re
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Laplace C.;
Submitted (I
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                             EMBL;
                                                                                                                                                                                                                                                         MEDIINE=20432087; PubMed=10974536;
Levy S.E., Chen Y.-S., Graham B.H., V.
"Expression and sequence analysis of
translocase 1 and 2 genes.";
Gene 254:57-66(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) ADP_ATP carrier protein, fibroblast isoform (Adenine nucleotide translocator 2) (ANT 2).
         EMBL; AF240003; AAF64471.1; -. MGD; MGI:1353496; Slc25a5.
                                                                                        entities
                                                                                                     the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                         This SWISS-PROT entry is copyright. between the Swiss Institute of Bioi
                                                                                                                                                                                                                                                                                                                                                                                            Costet P., Laplace C. Submitted (FEB-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97059403; PubMed=8903724;
Ellison J.W., Li X., Francke U.,
"Rapid evolution of human pseudoa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Adenine nucleotide translocator SLC25A5 OR ANT2.
                                                                               or send
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thesis (1995),
                                                                                                                                                                           SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                         SUBUNIT: Homodimer
                                                                                                                                                                                                                                     FUNCTION: CATALYZES THE EXCHA
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                   U10404; AAA19009.1;
X70847; CAA50196.1;
AF240003; AAF64471.1
                                                       U27316; AAC52838.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome 7:25-30(1996).
                                                                                an email to license@isb-sib.ch).
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                                                                                            requires a license
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                                                                                                                                                                                                                                                                                                                                             (FEB-1997)
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Rodentia;
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pseudoautosomal gene
                                                                                            agreement
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                                                                                                                ght. It is produced through a collak Bioinformatics and the EMBL outer titute. There are no restrictions ns as long as its content is in
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InterPro; IPR002030; Mit_uncoupling
InterPro; IPR001993; Mitoch_carrier

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Best Local S
Matches 271
                                                                                                                                                                                                                                                                      ADT1 RAT
Q05962;
01-FEB-1994
                                                     STRAIN-Sprague-Dawley, and Wistar; TISSUE-Hear MEDLINE-94002161; PubMed-8399300; Shinohara Y., Kamida M., Yamazaki N., Terada H. "Isolation and characterization of cDNA clones encoding rat mitochondrial adenine nucleotide Biochim. Biophys. Acta 1152:192-196(1993).

-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AN MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM TRANSMEM TRANSMEM
                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
SLC25A4 OR ANT1.
                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00153; mito carr; 3. PRINTS; PR00926; MITOCARRIER
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                     Rattus norvegicus (Rat)
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inner membrane.
TISSUE SPECIFICITY: I
EXTENT, IN BRAIN AND
                                 SUBCELLULAR LOCATION: Integral
                                              SUBUNIT: Homodimer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKRTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                             STANDARD;
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91.6%;
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                                                                                                                                   and Wistar; TISSUE=Heart,
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              N
   KIDNEY
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          HEART,
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Pred. No. 1.
                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
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            SKELETAL MUSCLE
                                   membrane
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                                                                                                             Terada H.;
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                                 protein.
                                                                   AND
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translocator.";
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                                                                  ATP
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            AND
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RESULT 7
ADTI MOUSE STANDARD; PRT; 298 AA.

AC P49962; Q62164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP,ATP carrier protein, heart/skeletal muscle i
translocase 1) (Adenine nucleotide translocator
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Best Local S
Matches 267
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REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X61667; CAA43842.1; -.
EMBL; D12770; BAA02237.1; -.
PIR; I60173; I60173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                   Mus musculus (Mouse)
                                                SLC25A4 OR ANT1 OR ANC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
                                                                                                                                                                                                                                                              VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSMMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
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32989 MW;
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           Chordata;
Rodentia;
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Pred. No. 1e-11
18; Mismatches
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Sciurognathi; Muridae;
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1e-117;
13;
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                                                             e isoform 7
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           Euteleostomi; 
Murinae; Mus
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                                                             (ADP/ATP) (mANC1).
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RA Strausberg R.D., Feingeld E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA RA RA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Bakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Bakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Bouterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RG "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 9916899-16903 (2002).
                                                                                                                                                                                                                                                                                     entities
or send a
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mit_ch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                        EMBL;
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TISSUE=Ey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.; "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ellison J.W., Li X., Francke U., Shapiro I "Rapid evolution of human pseudoautosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: CATALYZES THE EXCHANGE MITOCHONDRIAL INNER MEMBRANE. SUBUNIT: Homodimer.
                                                                                                                                                                    L; U27315; AAC52837.1; -.
L; X74510; CAA52616.1; -.
L; AF240002; AAF64470.1; -.
L; BC003791; AAH03791.1; -.
L; BC026925; AAH26925.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                ; BC026925; AAH26925.1
S37210; S37210.
MGI:1353495; Slc25a4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inner membrane
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Best Local Simi
Matches 265;
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01-JUL-1993
16-OCT-2001
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P02722;
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDIJINE=89229093; PubMed=2540808;
Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
"Two bovine genes for mitochondrial ADP/ATP translocase
differences in various tissues.";
Biochemistry 28:866-873(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOVIN
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REPEAT
                   MEDLINE=86295775; PubMed=3017341; Rasmussen U.B., Wohlrab H.;
                                                                                               mitochondria.";
Hoppe-Seyler's
                                                                                                                                       MEDLINE=82188267; PubMed=70761
Aquila H., Misra D., Eulitz M.
"Complete amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLC25A4 OR ANT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, heart isoform T1 (AD
(Adenine nucleotide translocator 1) (ANT 1).
                                                           SEQUENCE OF 207-297 FROM
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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cid sequence of the ADP/ATP
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                                                                                                     363:345-349(1982)
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between
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PRINTS; PR00926; MITOCARRIER.
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TION: CATALYZES
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Res. Commun. 138:850-857(
LYZES THE EXCHANGE OF ADF
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CCERTER REPRESENTATION OF THE PROPERTY OF THE 
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Worley A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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Comi G.P., Keranen J., Pelto
"Role of adenine nucleotide
Science 289:782-785(2000).
                                                                              VARIANTS PEO PRO-114 AND MET-289.
MEDLINE=20385067; PubMed=10926541;
Kaukonen J. Juselius J.K. Tiranti
Comi G.P., Keranen J., Peltonen L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88041149; PubMed=2823266;
Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
"CDNA sequence of a human skeletal muscle ADP/ATP translocator:
of a leader peptide, divergence from a fibroblast translocator c
and coevolution with mitochondrial DNA genes.";
Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
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MEDLINE=89340499; PubMed=2547778;

Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,

Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,

Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;

"A human muscle adenine nucleotide translocator gene has four a located on chromosome 4, and is differentially expressed.";
                                                                                                                                                                                                                                                     Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are
level in adult human liver.";
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                                                                                                                                                                                                                                                                                                                                             MEDLINE=88124845; PubMed=2829183;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF
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Bumalia; Eutheria; Primates;
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15-SEP-2003 (Rel.
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translocase 1) (
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                                                                                                                                                                                                                                Acad.
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el. 16, Last sequence update)
el. 42, Last annotation update)
r protein, heart/skeletal muscle i
(Adenine nucleotide translocator
                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                             Sci. U.S.A.
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wick M.J., Walke
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MIM; 10.

R MIM; 157640;

R MIM; 157640;

R GO; GO:0005887; C:mitochon.

DR GO; GO:0005739; C:mitochon.

DR GO; GO:0005207; F:adenine transport.

GO; GO:0006091; P:energy pathways; TAS.

DR GO; GO:0000002; P:mitochondrial genome mainten.

DR GO; GO:0006832; P:small molecule transport; TAS.

DR GO; GO:0006832; P:small molecule transport; TAS.

DR GO; GO:0006832; Mit_uncoupling.

DR InterPro; IPR002030; Mit_uncoupling.

DR InterPro; IPR001993; Mitoch carrier.

PRINTS; PR00153; mito_Carr; 3.

PRINTS; PR00926; MITOCARRIER.

DR PRINTS; PR00926; MITOCARRIER; 3.

PROSITE; PS00215; MITOCH CARRIER; 3.

P
                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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EMBL; J03593; AAA36751.1; -.
EMBL; J04982; AAA51736.1; -.
EMBL; BC008664; AAH08664.1; -.
PIR; A44778; A44778.
Genew; HGNC:10990; SLC25A4.
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBURIT: Homodimer.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the mitochondrial carrier family.
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I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG
                             I PKEQGVLS FWRGNLANVIRYF PTQALNFA FKDKYKQI FLGGVDKHTQFWRYFAGNLASG
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V -> M (IN PEO).

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KGA -> RR (IN REF. 3).

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Annanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards Q., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harlis N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase) (AdT) (Stress sensitive B protein).
SESB OR A/A-T OR CG16944.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Oregon-R;
Zhang Y.Q., Davis A.W.,
Submitted (JAN-1997) to
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MEDLINE=20196006; PubMed=10731132;
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"Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila.";
Experientia 50:749-762(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanogaster shows a high degree ADP/ATP translocases.";
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NCBI_TaxID=7227;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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cDNA clone encoding the ADP/ATP translocase of Drosophila
lanogaster shows a high degree of similarity with the mamma
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the EMBL/GenBank/DDBJ or
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A Liasko P., Lei Y., Levitsky A.A., Li J., Li J., Liang Y., Lin X.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Pacleb J.M.,
A Melson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Shen H.,
A Palazzolo M., Pittman G.S., Simpson M., Skupski M.P., Smith T.,
A Reinert K., Reminojton K., Saunders R.D.C., Scheeler F., Shen H.,
A Reinert K., Reminojton K., Saunders R.D.C., Scheeler F., Smith T.,
A Spier B., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier B., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Spier B., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Yellong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.
The genome sequence of Drosophila melanogaster.",
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REMBL; S71762; AAB31734.3; -.

REMBL; Y10618; CAA71628.1; -.

REMBL; AB2003484; AAF49557.1; -.

REMBL; AY000978; AAL25526.1; -.

REMBL; AY070894; AAL48516.1; -.

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SEQUENCE FROM N.A.
STRAIN=Berkeley; TISSUE=Larva, Ovary, and
MEDLINE=22426086; PubMed=12537569;
Crapleton M., Carlson J.W., Brokstein P.,
Crapleton M., Carlson J.W., Dromiller B., Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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George A., Guarin H., Kronmiller B., Pacl
Rubin G.M., Celniker S.E;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.
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between the
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DOMAIN: Composed of three homologous domains.

SIMILARITY: Belongs to the mitochondrial carrier family.
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M., Park S.,
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leb J.M.,
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O1-NOV-1997 (Rel. 35, Created)

O1-NOV-1997 (Rel. 35, Last sequence update)

O1-NOV-1997 (Rel. 35, Last annotation update)

T 01-NOV-1997 (Rel. 35, Last annotation update)
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94348635; PubMed=8069414;
Beard C.B., Crews-Oyen A.E., Kumar V.K.,
"A cDNA encoding an ADP/ATP carrier from
gambiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; In
Neoptera; Endopterygota; Diptera; Nematocera
NCBI_TaxID=7165;
                        PROSITE; rousses, Inner membrane;
                                                 Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARR
                                                                                                                   EMBL; L11618; AAB04104.1; -. EMBL; L11617; AAB04105.1; -.
                                                                                        InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                        Insect Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                              FUNCTION: CATALYZES THE EXCHANGE O
MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: Homodimer (By similarity)
                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the mitochondrial carrier family.
                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                                                            s requires a license agreement (Se an email to license@isb-sib.ch).
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orane; Repeat; Transmembrane;
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era; Culicoidea;
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01-JUL-1993 (Rel. 26, Last sequer
15-JUL-1998 (Rel. 36, Last annote
ADP,ATP carrier protein (ADP/ATP
                                                                                                                                                                                     entities requires a license agreement (for send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
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Chlorella kessleri.
                                                                  InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carri
                                                                                                                  EMBL; M76669; AAA33027.1; -. PIR; A41677.
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                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHLKE
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                                                                         Feldmann H., Mannhaupt G., S
Submitted (AUG-1994) to the
-!- FUNCTION: CATALYZES THE
                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ADP_ATP carrier protein 3 (ADP/ATP translocase translocator 3) (ANT 3).
                                                                                                        STRAIN=S288c;
                                                                                                                                            Submitted
                                                                                                                                                                                                          MEDLINE=90324269; PubMed=2165073;
Kolarov J., Kolarova N., Nelson N.;
"A third ADP/ATP translocator gene in
J. Biol. Chem. 265:12711-12716(1990).
                                                                                                                                                                                                                                                                                                                                                                            P18238;
01-NOV-1990
                                                                                                                     SEQUENCE OF 38-307
                                                                                                                                                                          STRAIN=S288c;
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                       AAC3 OR YBR085W OR YBR0753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion;
        DOMAIN: COMPOSED SIMILARITY: Belon
                                        SUBCELLULAR LOCATION: Integral
                                                 SUBUNIT: Homodimer
                                                              MITOCHONDRIAL INNER MEMBRANE
                             inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                  _YEAST
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                                                                                                                                           (AUG-1994) to
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     POSED OF THREE HOMOLOGOUS DOMAINS Belongs to the mitochondrial
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                                                                        Schwarzlose C., Vetter e EMBL/GenBank/DDBJ data E EXCHANGE OF ADP AND AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
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Pred. No. 1.6e
26; Mismatches
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(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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                                                                                                                                                              Jauniaux J.C., Urrestarazu
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                                          membrane
                                                                                                                                                                                                                                                                                                                                                                                                   307
                                                                                                                                                                                                                     yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Transport
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.6e-78;
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                                        protein.
                                                                         BJ databases
AND ATP ACR
          carrier
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                                                                          ACROSS
                                           Mitochondrial
          family
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There are no restrictions ing as its content is in

a collaboration

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RESULT 14
ADT_CHLR
ID ADT C
ID ADT C
P2708
DT 01-AU
DT 01-AU
DT 01-AU
DT 01-Q
DE ADD, C
DE ADT, C
GN ABT.
GN ABT.
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COC NCBI
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Best Local S
Matches 161
                                                                                                                                                         P27080;
P27080;
O1-AUG-1992 (Rel. 23, C
O1-AUG-1992 (Rel. 23, I
O1-OCT-1994 (Rel. 30, I
                                                                                                                         01-OCT-1994 (Rel. 23, Last sequence update)
ADP,ATP carrier protein (ADP/ATP translocase)
translocator) (ANT).
                                                                           Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales.
Chlamydomonadaceae; Chlamydomonas.
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SGD; S0000289; AAG3.
GO; GO:0005471; F:ATP/ADP antiporter activity; IMP.
GO; GO:0006854; P:ATP/ADP exchange; IMP.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                          SEQUENCE FROM N.A.
STRAIN=FUD44-R2;
             MEDLINE=93204887; PubMed=8455552;
                                                              NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Multigene fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER;
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M34076; AAA97485.1; -. EMBL; Z35954; CAA85031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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53.7%;
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Pred. No. 4.
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JSULT 15
ADT SCHPO
ID ADT SCHPO
AC Q09188;
DT 01-NOV-1997 (Rel. 35,
DT 28-FEB-2003 (Rel. 41, La.
T 28D,ATP Carrier protein (A)
"translocator) (ANT).
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Best Local
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TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translocator gene from Chlamydomonas
MO1. Genet. 237:134-144(1993).
-i- FUNCTION: CATALYZES THE EXCHANGE
MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
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InterPro; IPR001993; Mitoch_carri
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SUBCELLULAR LOCATION: Integral membrane
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                                                                                                                                                                                                                             KVI 298
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                                                                     (Rel. 35, Last sequence update)
(Rel. 41, Last annotation updat
rier protein (ADP/ATP translocas
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Pred. No. 1.
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											Matches	Query Match	SEQUENCE	TRANSMEM	TRANSMEM	TRANSMEM	TRANSMEN
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•	TSGEAVKYSSSFECGRQILAKEGARSFFKGAGANILRGVAGAGVLSIYDQVQ 314	QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAMSNVLRGMGGAFVLVLYDELK	GIVVYR	GIIIYR	AASLLF	ATSLCF	EGVISL	QGVLSF	FFFDFM	FAKDFL	= 5		322 AA;	289	222	197	131
	-VKYS	TYMIG	GLYFC	AAYFG	AYSTE	TAAA	WRGNI	WRGNI	MGGVS	AGGIA	vat			309	242	21	151
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	GRQIL	WRKIE	KPVVL	KG-ML	LANDA	LAADV	YFPTQ	YFPTC	TAAAP	TAVAP			MW;	σ	ហ	4.	ω
	AKEGA	RDEGG	VGPLE	PDPKN	KSAKK	GKS	ALNFA	ALNEA	IERVK	IERVK	; Mismat	Score 769;	8AC3D	(POTE	(POTE	ETOG)	(POTE
	RSFFKC	CAFFKC	ENFLAS	HIVVS	GERQI	TERE	FKDKFI	KOKY	TION	TLOV		69;	16A40I	(POTENTIAL)	(POTENTIAL)	(POTENTIAL)	(POTENTIAL)
	ARSFFKGAGANILRGVÆ	AWSNV	SFLLGW	WMIAQ	NGLVD	RGLGD	KFKKMF-G	QIFLG)DEM)HASKQ	hes 75;	DB 1;	8AC3D16A40F41AFC	•	•	•	•
	LRGVA	LRGMG	AVITG	TVTAV	VYRKT	CLVKI'	YKKER	GVDKH'	IRAGR	IAADK		Length	CRC64;				
	GAGVL	GAFVL'	SGVAS	AGVVS	YRSDGI	TKSDG	DGYAKWI	TQFWR.	LSHRY	QY	Indels	th 322	4 ;				
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Search completed: December 18, 2003, 17:09:02 Job time : 18 secs

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       ADP, ATP carrier
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344.5	363	368	369.5	370.5	372	381	383	520.5	681.5	734.5	737.5	739.5	742	742.5	743
22.3	23.5	23.8	23.9	24.0	24.1	24.7	24.8	33.7	44.2	47.6	47.8	47.9	48.1	48.1	48.2
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GLGDCLVKITKSDGIRGLYQGFSVS 180	KQIFLGGVDKHTQFWRYFAGNLASG 120 	LQVQHASKQIAADKQYKGIVDCIVR 60 	DB 1; Length 298; 129; 0; Indels 0; Gaps 0;	:403000 ment of sequences for GDB:ANT2 and GDB: arrier protein repeat homology ; transmembrane protein predicted <amt> ology <acp1> homology <acp2> homology <acp3></acp3></acp2></acp1></amt>	AAA36750.1; PID:g339723	se are expressed at the mRNA level in a 829183	enes for human mitochondrial ADP/ATP tr 541251 n	sidentification); mitochondrial ADP,ATP 0 #text_change 17-Mar-2000		hypothetical prote ADP/ATP translocas hypothetical prote mitochondrial solu hypothetical prote hypothetical prote hypothetical prote hypothetical prote peroxisomal Ca-dep probable mitochond Ca-dependent solut

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ADP, ATP carrier protein T2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-
C;Accession: B43646
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Wallion Biochemistry 28, 866-873; 1989
B;Cthemistry 28, 866-873; 1989
A;Title: Two bovine genes for mitochondrial AD A;Reference number: A43646; MUID:89229093; PMID:A;Accession: B43646
A;Status: preliminary
A;Accession: A.J...A;Accession: A.J...A;Accession: A.J...A;Accession: A.J...A;Accession: A;Accession: Accession: Accessio: Accession: Accession: Accession: Accession: Accession: Accessi
                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence revision 17-M
C;Accession: A29132; C28116
R;Battini, R.; Ferrari, S.; Kaczmarek, L.;
J. Biol. Chem. 262, 4355-4359, 1987
A;Title: Molecular cloning of a cDNA for a A;Reference number: A29132; MUID:87166056; A;Accession: A29132
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A; Residues: 1-298
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Species: Bos primigenius taurus (cattle)
Date: 03-Mar-1993 #sequence_revision 03-Mar-1993
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Pred. No. 3.3e-126;
4; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                        human ADP/ATP
PMID:3031073
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A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: C28116
A;Molecule type: mRNA
A;Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HC
A;Cross-references: GB:J03591; NID:g339720; PIDN:AAA3674
A;Experimental source: Clone pHAT3
C;Genetics:
                                                                                                                                                                                  A;Introns: 37/3; 200/1; 247/1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords duplication; transmembrane protein
C;Keywords duplication; transmembrane protein
E;5-99/Domain: ADP,ATP carrier protein repeat homology <ACPl-
                                                                                                                                                                                                                                                                                                                                                                                                                 R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H. Biochim. Biophys. Acta 1152, 192-196, 1993 A;Title: Isolation and characterization of cDNA clones A;Reference number: I60173; MUID:94002161; PMID:8399300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
C;Accession: I60173
C;Schinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 (C;Superfamily: ADP,ATP carrier protein ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitcochondrion; transmembrane protein E;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
                                                                                                                                           F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Cross-references: GI
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Best Local Similarity
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267; Conserva
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89.6%;
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                                                            Score 1424; D
Pred. No. 2e-1
L8; Mismatches
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Pred. No. 4
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                                                                                 2e-118;
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#status

experimental

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A;Molecule type: protein
A;Residues: 205-298 <BAB->
R;Oettmeier, W.; Masson, K.; Kalinna, S.

Eur. J. Biochem. 227, 730-733, 1995
A;Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial A;Teference number: S69369; MUID:95172058; PMID:7867632
A;Accession: S69369
A;Accession: S69369
A;Molecule type: protein
A;Residues: 49-631544-168 <OET>
C;Comment: This protein is synthesized in the cytosol and transported into the mitoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP,ATP carrier protein T1 - bovine

N;Alternate names: ADP/ATP translocase T1
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence revision 22-Jul-1994 #text_change
C;Accession: A43646; A24822; A03181; A61343; S69369
C;Accession: A43646; A24822; A03181; A61343; S69369
R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
Biochemistry 28, 866-873, 1989
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase
A;Reference number: A43646; MUID:89229093; PMID:2540808
A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial A;
A;Note: located in the inner mitochondrial membrane
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid.
F;S-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 2-51, X', 53-70, X', 72-109, 'X', 111-298 < AQU>
A; Residues: 2-51, E may be methyllysine
A; Note: residue 52 may be methyllysine
R; Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A; Title: Amino acid sequence determination of the ADP, ATP
A; Reference number: A61343; MUID:82046808; PMID:6271240
A; Accession. A61343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Medecule type: mRNA
A; Residues: 208-298 cARS,
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
A; Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1;
R; Aquila, H.; Misra, D.; Bulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A; Title: Complete amino acid sequence of the ADP/ATP carrier
A; Reference number: A03181; MUID:82188267; PMID:7076130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier:
A;Reference number: A24822; MUID:86295775; PMID:3017341
A;Accession: A24822
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C;Accession: S37210
R;Laplace, C.; Costet, P.
submitted to the EMBL Data
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                                                                                                                                                                                                                                                                                                                                                                                                                                       F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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C;Genetics:
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A; Accession: S37210
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Best Local
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                                                                                                                                  GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
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Pred. No. 6
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Mismatches 13;
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A;Gende: GDB:ANT1; T1
A;Gende: GDB:ANT1; T1
A;Cross-references: GDB:119680; OMIM:103220
A;Cross-references: GDB:119680; OMIM:103220
A;Map position: 4q35-4q35
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein F;2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F;2-298/Product: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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R;Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A;Title: Two distinct genes for ADP/ATP translocase are
A;Reference number: A94197; MUID:88124845; PMID:2829183
A;Accession: A28116
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A;MoHecule type: DNA
A;Residues: 1-298 CCOZ>
R;Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A;Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of A;Reference number: A39891; MUID:88041149; PMID:2823266
A;Accession: A39891.
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J. Mol. Biol. 206, 261-280, 1989
A;Title: DNA sequences of two expressed nuclear genes for
A;Reference number: S03893; MUID:89236396; PMID:2541251
A;Accession: S03893
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A;Molecule type: DNA
A;Residues: 1-298 <LIA>
A;Residues: 1-298 <LIA>
A;Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1;
A;Ccosns, A.L.; Runswick, M.J.; Walker, J.E.
T. 10.1 20.0 1000
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N;Alternate names mitochondrial ADP,ATP translocase 1

C;Species: Homo sapiens (man)

C;Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text_change 17-Mar-2000

C;Accession: A44778; S03893; \overline{A39891; A28116}

R;Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.

J. Biol. Chem. 264, 13998-14004, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-15,'A',17-146,'RR',149,151-226,'L',228-298 <NEC>
A;Cross-references: GB:J02966; NID:G339919; PIDN:AAA61223.1; P
A;Experimental source: clone pHMANT
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A;Cross-refe
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A; Residues: 1-37 < HOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                           121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                    263;
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                               GAAGATSLCFVYPLDFARTRLAADVGKGAAQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                                                                                                                                                                                                                I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             91.3%; Score 1409; DB 1;
88.3%; Pred. No. 4.3e-117;
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C;Date: 10-Sep-1
C;Accession: S31
R;Beard, C.B.; (
A;Molecule type: DNA
A;Residues: 1-301 <BEA
A;Cross-references: EMBL:221814; EMBL:221815
A;Cross-references: EMBL:221814; EMBL:221815
C;Superfamily: ADP,ATP carrier protein; ADP,ATI
C;Keywords: duplication; transmembrane protein
F;7-101/Domain: ADP,ATP carrier protein repeat
                                                                                                                                                                                                                                                                      R;Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H. submitted to the EMBL Data Library, February 1 A;Description: A cDNA encoding an ADP/ATP carr
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ADP,ATP carrier protein - African malaria mosquito C;Species: Anopheles gambiae (African malaria mosquito) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #tex C;Accession: S31935; S31936

#text_change 10-Sep-1999

A; Reference number: A; Accession: S31935

S31935

February 1993

carrier

from

the

mosquito Anopheles gambiae

A;Status: preliminary

ADP, ATP carrier protein

repeat homology

homology <ACP1>

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A;Reference number: S31814
A;Accession: S31814
A;Accession: S31814
A;Accession: S31814
A;Accession: S31814
A;Accession: S1816
A;Accession: S1816
A;Accession: Speciment
A;Residues: 1-298 <COS>
A;Rosidues: 1-298 <COS>
A;Cross-references: EMBL:X70847
A;Cross-references: EMBL:X70847
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein
C;Keywords: duplication; transmembrane protein
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP1>
ACP1-202/Domain: ADP,ATP carrier protein repeat homology <ACP1>
ACP1-203/Domain: ADP,ATP carrier protein repeat homology <ACP1-203/Domain: ADP,ATP carrier protein repeat homology <ACP1-203/Domai
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N;Alternate names: adenine nucleotide translocase
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-199:
C;Accession: S31814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264;
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                                      QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
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QSGRKGTDIMYTGTLDCWRKIARDEGSKAFFKGAWSNVLRGMGGAFVLVLYDEIKK 296
                                                                                                                                                  VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIFISWMIAQSVTLVAGLTSYPFDTVRRRMM
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Pred. No. 9.8e-117;
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R;McMurray, A.
submitted to the EMBL Data Library, Dec.
A;Reference number: Z19707
A;Accession: T23207
A;Status: preliminary; translated from
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A; Introns: 4/1; 191/2
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A;Experimental source: clone K011
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F;209-300/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: ADP, ATP
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Best Local
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                                                                                                                                                                                                                       MTEQA--ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCI 58
                           ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI
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                                                                                                                                 LCFVYPLDFARTRLAADVGKA-NEREFKGLADCLVKIAKSDGPIGLYRGFFVSVQGIIIY
                                                                                                                                                                LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY
                                                                                                                                                                                                   AALWRGNLANVIRYFPTQALNFAFKDTYKNIFQKGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                  FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASLTIAADKRYKGIVDVLVRVPKEQGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSVQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGGAAGATSLCFVYPLDFARTRLGADVGPGAGEREFNGLLDCLKKTVKSDGIIGLYRGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRIPKEQGIGAFCGGNLANVIRYFPTQALNFAFKDVYKQVFLGGVDKNTQFWRYFLGNLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTKKADPYGFAKDFLAGGISAAVSKTAVAPIERVKLLLQVQAASKQIAVDKQYKGIVDCF
-DVLYKNTLDCAVKIIKNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFI
                                                                                                                                                                                                                                                                                                                                        Conservative
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77.0%;
                                                                                                                                                                                                                                                                                                                                   67.5%; Score 1041; DB 2; 70.9%; Pred. No. 1.7e-84; tive 29; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carrier protein repeat homology <ACP2>
carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.
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Pred. No. 3.
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3.6e-97;
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                                                                                                                                                                                                                                                                                                                                                                   Length 313;
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A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1
A;Experimental source: clone T27E9
C;Genetics:
A;Gene: CESP:T27E9.1
A;Map position: 3
A;Introns: 20/1; 41/3; 115/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homolog
                                                                                                                                                                                                                                                                                                                               hypothetical protein T27E9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000 C;Accession: T25371 R;Lloyd, C.
                                                                                                                                                                                                               A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-300 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 4
A; Introns: 4/1; 191/2
C; Superfamily: ADP, ATP
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                                                                                                                                                                                                                                                                      submitted to the EMBL Data A;Reference number: Z20024 A;Accession: T25371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-313 <GEI>
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  Matches
                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Local Similarity 69.:
mes 202; Conservative
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207; Conserv
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                67.3%;
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70.9%; Pred. No. 2.60
tive 29; Mismatches
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  37;
Score 1038; DB 2;
Pred. No. 3e-84;
7; Mismatches 49;
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                                    Length 300;
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A; Gene: CESP: W02D3.6
A; Map position: 1
C; Superfamily: ADP, ATI
F; 9-103/Domain: ADP, A'
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A;Molecule type: DNA
A;Residues: 1-300 <LET>
A;Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AAB54179.1; GSPDB:GN
A;Experimental source: strain Bristol NZ; clone W02D3
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid WO2D3
A;Reference number: 218308
A;Accession: T15206
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Best Local Similarity
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300
                                        298 I
                                                                                242
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                                                                                                                                                               VSVQGIIIYRAAYFGMFDTAKTLYSTDGQKLNFFTTWAIAQVGTVGSGYLSYPWDTVRRR
                                                                                                                                                                                    VSVQGIIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRR
                                                                                                                                                                                                                                               SGGAAGATSLCFVYPLDFVRTRLGADVGK-GVDREFQGLTDCFVKIVKSDGPIGLYRGFF
                                                                                                                                                                                                                                                                       SGGAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFS
                                                                                                                                                                                                                                                                                                                                ARVPKEQGYAAFWRGNLANVLRYFPTQALNFAFKDTYKKMFQEGIDKNKEFWKFFAGNLA
                                                                                                                                                                                                                                                                                                                                                     VRIPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                               TEQAISFAK---DFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAAYFGMFDTAKMVFASDGQKLNFFAAWGIAQVVTVGSGILSYPWDTVRRRMMQSGRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AALWRGNLANVIRYFPTQAMNFAFKDTYKAIFLEGLDKKKDFWKFFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGV
                                                                                MMMQSGRK--DILYKNTLDCVRKIVKNEGITALYKGGLSNVFRATGGALVLTIYDEIQHL
                                                                                                                                                                                                                                                                                                                                                                                                             TKEGFDYRKFLVDLASGGTÄÄÄISKTÄVÄPIERVKLLLQVSDVSETVTÄDKKYKGIMDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DILYKNTLDCAKKIIQNEGMSAMFKGALSNVFRGTGGALVLAIYDEIQKFL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLIDLASGGTAAAVSKTAVAPIERVKLLLQVQDASKAIAVDKRYKGIMDVLIRVPKEQGV
                                        298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.4%; Score 993.5; 64.8%; Pred. No. 2.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.6e-80;
ches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 14

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7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAAD--KQYKGIVDCIVRIPKE

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C;Keywords: duplication; transmembrane protein F;6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;112-203/Domain: ADP,ATP carrier protein repeat homology <ACPF;209-301/Domain: ADP,ATP carrier protein repeat homology <ACPF;209-301/Domain: ADP,ATP carrier protein repeat homology <ACPF;209-301/Domain: ADP,ATP carrier protein repeat homology <ACPF
                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-301 <HA'
                                                                                                                                                                                                                                                                                                                                                                             A; Title: Molecular characterisation of the ADP/ATP-transporter cDNA A; Reference number: S68993; MUID:95188918; PMID:7883016
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S68993; S51132
R;Hatin, I.; Jaureguiberry, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum)
N;Alternate names: ADP/ATP transporter
C;Species: Plasmodium falciparum
C;Species: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M76669; NID:9516596; PIDN:AAA33027.1; PID:9516597 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Glucose increases the expression of the ATP/ADP A; Reference number: A41677; MUID:92084708; PMID:1748677 A; Accession: A41677
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C;Species: Chlorella Kessleri
C;Date: 30-Jun-1992 #sequence_revision
C;Accession: A41677
                                                                                                                                                                                                           A;Cross-references: EMBL:X83551; NID:g623334; PIDN:CAA58541.1; PID:g623335
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat home
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A; Residues: 1-339 <HIL>
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J. Biol. Ch
                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                 A; Accession: S68993
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Matches
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Chem. 266, 24044-24047, 1991
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                                                                                                                                                                                                                                                                      1-301 <HAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADK--QYKGIVDCIVRIPK
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                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIIYRAAYFGVYDTAKGML-PDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQGVASFWRGNLANVVRYFPTQAFNFAFKDTIKGLFPKYSPK-TDFWRFFVVNLASGGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GGERQYNGTIDCWRKVAQQEGMKAFFKGAWSNVLRGAGGAFVLVLYDEIKKFI 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                     228, 86-91,
Conservative
                         61.1%;
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                         Score 943; DB 2;
Pred. No. 7.6e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 978; DB 2; Pred. No. 7.1e-79;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-Jun-1992 #text_change 20-Aug-1999
                                                                                                    homology <ACP2>
homology <ACP3>
                                               Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 339
  Indels
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Search completed: December 18, 2003, 17:11:23 Job time : 21 secs	246 RKGKEEIQYKNTIDCWIKILRNEGFKGFFKGAWANVIRGAGGALVLVFYDELQKLI 301	244 RKG-ADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298	186 IVYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPFDTVRRRMMMMSG 245	185 IIYRAAYEGVYDTAKGML-PDPKNTHĬVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSG 243	127 AISLLIVYPLDFARTRLASDIGK-GKDRQFTGLFDCLAKIYKQTGLLSLYSGFGVSVTGI 185	125 ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI 184	68 QGVLSLWRGNVANVIRYFPTQAFNFAFKDYFKNIF-PRYDQNTDFSKFFCVNILSGATAG 126	65 QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124	8 NFAADFLMGGISAAISKTVVTPIERVKMLIQTQDSIPEIKSGQVERYSGLINCFKRVSKE 67

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Match
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Q9PRH1
Q9PRH2
Q9Y1C4
Q9SVX4
Q9SVX4
Q9S1336
Q9F1336
Q9F1336
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      Q9i9m9 xenopus lae
Q8bvi9 mus musculu
Q9pxh1 rana rugosa
Q9pxh2 rana rugosa
Q9yic4 rana rugosa
Q9yic4 rana rugosa
Q9yic4 rana sylvat
Q91336 rana sylvat
Q8ira0 drosophila
Q9inw5 lucilia cup
Q44093 drosophila
                                                                                                   QBaym3 gallus gall
QBsgh5 bos taurus
QBjhiO brachydanio
O46373 oryctolagus
Q919m9 xenopus lae
Q25129
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
749	753	756.5	759	760	764	767.5	778.5	827	924	924	932	936	943	944	944	946.5	947	973.5	993	993.5	996	1036.5	1038	1039	1041	1119	1137.5	1159
48.5	48.8	49.0	49.2	49.3	49.5	49.7	50.5	53.6	59.9	59.9	60.4	60.7	61.1	61.2	61.2	61.3	61.4	63.1	64.4	64.4	64.5	٠	67.3	67.3	•	72.5	73.7	75.1
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Q8j0u1 gaeumannomy	Q26697 trypanosoma	caenorh	074260 candida par	076286 trypanosoma		Q8j0m2 yarrowia li	Q9p8m1 yarrowia li		Q8mvr6 nyctotherus	Q8mvr5 nyctotherus	Q8mvr8 nyctotherus	Q8mvr7 nyctotherus	Q26006 plasmodium	Q8mvr4 euplotes sp	Q25692 plasmodium				Q17407 caenorhabdi	001813 caenorhabdi	α.	7	O45865 caenorhabdi	P91410 caenorhabdi			O62526 drosophila	Q8bkq5 mus musculu

ALIGNMENTS

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121 GAAGATSLCFYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180	61 IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120 	1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR 60 -	Query Match 95.5%; Score 1474; DB 13; Length 298; Best Local Similarity 93.0%; Pred. No. 2.5e-125; Matches 277; Conservative 14; Mismatches 7; Indels 0; Gaps 0;	SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;	EBBS Lett. 0:0-0(2002).	"Cold-induced mitochondrial uncoupling and expression of chicken UCP and ANT mRNA in chicken skeletal muscle.";	M., Sato S., Seki Y., Sato K., Akiba Y.;	SECULENCE ERON N P	NCBI_TaxID=9031;	Gallus.	викагуога; месагоа; спогоага; стапіага; verrebrara; вителеовтомі; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	AVANT.	P antiporter.	rel.	23, Creat	Q8AYM3 PRELIMINARY; PRT; 298 AA.	3 1

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Q8JHI0;
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01-JUN-2002
01-JUN-2002
01-MAR-2003
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"Structural properties of mammalian mitochondrial ADP/ATP carriers:

"dentification of possible amino acids that determine functional differences in its isoforms.";

Mitochondrion 1:371-379(2002).

EMBL; ABM6543; BAB84673.1;

InterPro; IPR001993; Mitoch_carrier.

Pfam; PF00215; mito_carr; 3.

PROSITE; PS00215; MITOCH_CARRIER; 3.

SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;
     Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adenine nucleotide translocator 2.
                                                                                                                          Solute carrier
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92.2%;
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Teleostei;
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Pred. No. 3e-123;
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                            Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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MEDLINE 2203592; PubMed=12006978;

A Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E. Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Ni Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Ni Hopkins N.;

A Hopkins N.;

"Insertional mutagenesis in zebrafish rapidly identifies gen essential for early vertebrate development.";

L Nat. Genet. 31:135-140(2002).

R Mat. Genet. 31:135-140(2002).

R EMBL; AF506216; AAM34660.1; -.

R InterPro; IPR001993; Mitoch_Garrier.

R InterPro; IPR002067; Mit_uncoupling.

R PINTS; PR00153; mito_carr; 3.

R PFANTS; PR00926; MITOCHER.

R PRINTS; PR00926; MITOCHER.

R PRINTS; PR00784; MITOCH CARRIER.

R PRINTS; PR00784; MITOCH CARRIER; 3.

SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;
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rabbit which PRELIMINARY;

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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A., Khosrowshahian F., Varmuza S.L., Liversage R.

T "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specify

UT Dynamic Patterns of Expression During Development.";

L Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

C -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY

DR InterPro; IPR001993; Mitoch carrier.

DR InterPro; IPR002067; Mit_carrier.

DR InterPro; IPR002030; Mit_uncoupling.

DR Pfam; PF00153; mito_carr; 3.

DR Pfam; PF00153; mito_carr; 3.

DR PRINTS; PR00726; MITOCH_CARRIER; 3.

DR PRINTS; PR00726; MITOCH_CARRIER; 3.

R PROSITE; PS00215; MITOCH_CARRIER; 3.

KW Membrane; Transmembrane; Transport.

KW Membrane; Transmembrane; Transport.
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Q919M9;
01-OCT-2000
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Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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Membrane;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Adenine nucleotide translocase.
                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xer
NCBI_TaxID=8355;
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; Transmembrane; Transport.
298 AA; 32901 MW; CAEA32C88164AD78
                   I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYLDELKKVI 298
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I PKEQGFVSFWRGNLANVIRYFPTQALNFAFKDKYKKIFLDNVDKKTQFWRYFAGNLASG
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                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus.
                                                                                                                           92.1%;
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                                                                                                             Score 1421; DB 13;
Pred. No. 1.6e-120;
4; Mismatches 15;
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Pred. No. 1.3e-120;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                       Varmuza S.L., Liversage R.A. locase mRNA Exhibits Specific
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RESULT
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O1
O1
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OC
A

Q9PRH1 Q9PRH1;

PRELIMINARY;

298

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7

01-MAY-2000 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. ADP/ATP translocase.

13, 13, 23,

Created)
Last sequence update)
Last annotation updat

update)

Rana rugosa (Wrinkled frog). Eukaryota; Metazoa; Chordata;

Amphibia; Batrachia;

Anura;

Neobatrachia;

Vertebrata; a; Ranoidea;

Euteleostomi; Ranidae; Rana

Craniata;

밁 S 밁 Ś 밁 Ś В 5 밁 Ś

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RESULT
Q8BV19
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01-MAR-2003 (TrEMBLrel. 23, La.
Fr 01-MAR-2003 (TrEMBLrel. 23, La.
B Solute carrier family 25.
S Mus musculus (Mouse).
S Mus musculus (Mouse).
S Musculus (Mouse).
S Musculus (Mouse).
Chordata; Co
Mammalia; Eutheria; Rodentia; Sc
NCBI_TaxID=10090;
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Best Local S
Matches 264
                                                                                                                                                                                                                                                                                                                                                                                                                   the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation," 770 full-length cDNAs."; Nature 420:563-573 (2002).

EMBL; AK078077; BAC37117.1; -. SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;
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01-MAR-2003
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MEDLINE=22354683; PubMed=12466851;
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                                                                                    VQGIIIYRAAYFGVYDTAKGMLPDPKVTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                       GAAGATSLCFVYPLDFARTRLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                              GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRWM
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llarity 88.6%;
Conservative 20
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Pred. No. 6.8e
20; Mismatches
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Sciurognathi; Muridae;
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Murinae; Mus
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RESULT

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X MEDLINE=99081429; PubMed=9866197;

A Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;

T "The origin and differentiation of the heteromorphic sex chro
T Z, W, X, and Y in the frog Rana rugosa, inferred from the seq
T a sex-linked gene, ADP/ATP translocase.";

L Mol. Biol. Evol. 15.1612-1619(1998).

C -!-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

R EMBL; AB008463; BAA36513.1; --

R EMBL; AB008466; BAA36511.1; --

NR EMBL; AB008461; BAA36511.1; --

NR EMBL; AB008462; BAA36512.1; --

NR InterPro; IPR002030; Mit_och_cbrrier.

DR InterPro; IPR002030; Mit_och_cbrrier.

DR InterPro; IPR002030; Mit_ocupling.

PFAINTS; PR00926; MITOCARRIER.

DR PRINTS; PR00926; MITOCARRIER.

DR PRINTS; PR00784; MTUNCOUPLING.

DR PROSITE; PS00784; MTUNCOUPLING.
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Best Local Similarity
Matches 264; Conserv
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Q9PRH2;
01-MAY-2000
MEDIJINE=99083429; PubMed=9866197;
Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh
"The origin and differentiation of the heteromorphic s
Z, W, X, and Y in the frog Rana rugosa, inferred from
a sex-linked gene, ADP/ATP translocase.";
Mol. Biol. Evol. 15.1612-1619(1998).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER F
EMBL; AB008458; BAA36509.1; -.
EMBL; AB008459; BAA36509.1; -.
                                                                                                                                                                                                                                                                                                                                                                       Rana rugosa (Wrinkled frog).
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; N
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01-MAR-2003
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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(TremBLrel. 13, Last seq
(TremBLrel. 23, Last ann
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                                                                                                                                                                                                                                                                                                                                                                          a; Craniata; Vertebrata; Euteleostomi;
Neobatrachia; Ranoidea; Ranidae; Rana
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Pred. No. 1
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annotation update)
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L.9e-119;
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                                                    z, W, x, and Y in the frog Rana rugosa, inferred from the a sex-linked gene, ADP/ATP translocase.";

Mol. Biol. Evol. 15:1612-1619(1998).

-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMI.

EMBL; AB008457; BAA36507.1; -.

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002067; Mit carrier.

InterPro; IPR002030; Mit_uncoupling.

Pfam; PF00153; mitocarriar.

PRINTS; PR00926; MITOCARRIER.

PRINTS; PR00926; MITOCARRIER.

PROSITE; PS00215; MITOCARRIER; 3.

Membrane; Transmembrane; Transport.

SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;
  Matches
              Query Match
Best Local
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Best Local
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR002030; Mit_uncoupling.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR007926; MITOCARRIER.
PRINTS; PR007984; MTUNCOUPLING.
PRINTS; PR007981; MTUNCOUPLING.
PROSITE; PS000215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 298 AA; 33082 MW; B0E225E
                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordāta; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
NCBI TaxID=8410;
                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                        Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.; "The origin and differentiation of the heteromorphic sex chromosomes
                                                                                                                                                                                                                                                                                                                                                                      Rana rugosa (Wrinkled frog)
                                                                                                                                                                                                                                                                                                                                                                                   ADP/ATP translocase.
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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298 AA; 33082 MW;
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  Conservative
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90.9%; Sco
87.9%; Pro
tive 21;
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Pred. No. 3.6e-1
20; Mismatches
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Last annotation updat
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  Score 1402; DB 13;
Pred. No. 8.3e-119;
1; Mismatches 15;
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Ranidae; Rana
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AC Q95VX
AC Q95VX
DT 01-DE
DT 01-DE
DT 01-MA
DF ADP-A
OS Ethmo
OC Eukar
OC Pleux
OX NCBI
RN [1] -
RN [1] -
RN SEQUE
RA BUTNE
RT "Nucl
RT "Ucl
RT TUDTI
RI SUBMI
DR EMBL;
DR Inter
DR Inter
DR Pfam;
DR PROSI
SCQUE
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Best Local Similarity 81.9
Matches 243; Conservative
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Q95VX4;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ da EMBL; AF401758; AALO2100.1; -.
EMBL; AF401758; AALO2100.1; -.
InterPro; IFR001993; Mitoch_carrier.
InterPro; IFR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PR00926; MITOCARRIER.
PROSITE; PR00926; MITOCARRIER; 3.
"SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ethmostigmus rubripes.
Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda; Pleurostigmophora; Scolopendromorpha; Scolopendridae; NCBI_TaxID=62613;
        Q91336
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Q8IRA0;
01-MAR-2003
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CG16944-PC.
                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Haxapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Membrane; Transmembrane; Transport.
SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cai Q., Storey K.B.;
Submitted (APR-1999) to tl
-l- SIMILARITY: BELONGS TO
EMBL; U44832; AAA97882.2;
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01-NOV-1996 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Cai Q., Greenway S.C., Storey K.B.;
"Differential regulation of the mitochondrial
in wood frogs under freezing stress.";
Biochim. Biophys. Acta 1353:69-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana sylvatica (Wood frog).
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Ne
NCBI_TaxID=45438;
SEQUENCE FROM N.A.
                             NCBI_TaxID=7227;
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TO THE MITOCHONDRIAL CARRIER FAMILY
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Pred. No. 8.2e-106;
19; Mismatches 17;
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eobatrachia; Ranoidea;
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MEDLINE=20196006;

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A Adams M.D., Celniker S.E., Helt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Scherer S.E., Hilt R.A., Evans C.A., Golare R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Hilt R.A., Evans C.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Hilt R.A., Exhburner M., Henderson S.N., RA Evandon R.C., Rogers Y.H., Blazej R.G., Chang Q., Chen L.X., RA Burtin R.C., Rogers Y.H., Blazej R.G., Change M., Pfeiffer B.D., RA Abril J.F., Agbayani A., An H.J., Andrews-Ffannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayrakkaroglu L., Beasley E.M., RA Ballew R.M., Bosu A., Baxendale J., Bayrakkaroglu L., Beasley E.M., RA Ballew R.M., Bouch J., Bocher H., Calleu E., Center A., Chandra I., RA Burris K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gabart W.M., Glasser K., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N., Kallshi F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Renington K.A., Mixon K., Nusskern D.R., Sathn H., Shue B.C., Siden-Kiamos I., Simpson M., Skupsk M.P., Smith T., RA Rang A.H., Wassarman D.A., Weinstock G.M., Weissenbach J., Rang S.M., Wassarman D.A., Weinstock G.M., Weissenbach J., Rang S., Yao Q.A., Ye J., The Genome sequence of Drosophila melanogaster."; Shu X., Smith H.O., Science 287:2185-2195 (2000)
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A Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

A Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

A Banzon J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Perriera S., Frise B., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Hogona C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubbin G.M., Wungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AF218587; AAF32322.1; --
InterPro; IPR001993; Mitoch carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE003484; AAN09267.1; -. SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;
                                                                                                                                                                                                                        PRINTS; PR00926; MITOCARRIER; 3. PROSITE; PS00215; MITOCH_CARRIER; 3. Membrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SS mal
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Lucilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP/ATP translocase.
Lucilia cuprina (Greenbottle fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9NHW5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9NHW5
                                                                                                                                                                                                                                                                                                                                                             IN=SS mal seeking;
Z., Fair J.A., Ba
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126 TSLCFVYFLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGII
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                                                                                                                6 ISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQ
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                                                                                                                                                                      Similarity
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                                                            GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGR
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                                            GFASYWRGNMANVIRYFPTQALNFAFKDKYKQVFLGGVDKNTQFWRYFLGNLASGGAAGA
                                                                                                  LGFVKDFAAGGISAAVSKTAVAPIERVKLLLQVQHISKQISPDKQYKGMIDCFVRIPKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KATEVIYKNTLHCWATIAKQEGTGAFFKGAFSNILRGTGGAFVLVLYDEIKKVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Arthropoda;
                                                                                                                                                                                                                300 AA;
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
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                                                                                                                                                                                                                33036 MW;
                                                                                                                                                      80.1%; Sc
79.5%; Pr
tive 24;
                                                                                                                                                                                                                                                                                                                                                                   Batterham
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                                                                                                                                                                    Score 1235.5;
Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1254.5; DB 5; Pred. No. 2.1e-105;
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                                                                                                                                                                                                                5459DF0EA0E2E742 CRC64;
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hexapoda; Insecta; Pterygota;
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RESULT 15
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Best Local Similarity
Matches 230; Conserva
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InterPro; IPR001993; Mitoch Carrier.
InterPro; IPR001993; Mitoch Carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCHARRIER.
PROSITE; PS000215; MITOCH CARRIER; 3.
PROSITE; PS000215
   O44094;
O44094;
01-JUN-1998
01-JUN-1998
01-MAR-2003
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             044093
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                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.0%; Score 1187.5; DB 5; Length 80.7%; Pred. No..2.2e-99; tive 19; Mismatches 33; Indels
       06,
23,
Created)
Last sequence update)
Last annotation update)
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Best Local Sim
Matches 229;
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InterPro; IPR001993; Mitoch carrier.
InterPro; IPR002067; Mit carrier.
Pfam; PF00153; mito carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                Membrane; Repeat; Transmembrane; Transport.
NON_TER 288 288
SEQUENCE 288 AA; 31775 MW; 06AlD1E477E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zeng L.-W., Comeron J.M., Chen B., Kreitman Genetica 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila subobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF025799; AAB87884.1;
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                                                               | IIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGR
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KATEIIYKNTIHCWGTIAKQE-GTAFFKGAFSNVLRGTGGAFVLV
             KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLV
                                               ATSLCFVYPLDFARTRLAADTGKGG-QREFTGLGNCLTKIFKSDGLVGLYRGFGVSVQGI
                                                                                                                    ATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGI
                                                                                                                                                                     QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG
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31775 MW; 06A1D1E477E81B26 CRC64;
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80.4%; Pred. No. 5e-99;
tive 20; Mismatches
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Search completed: December 18, 2003, 17:09:58
Job time : 44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
protein - protein search, using sw model
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OM protein - protein search, using sw model

Run on: December 18, 2003, 17:10:04; Search time 31 Seconds (without alignments) 1795.292 Million cell updates/sec

Title: US-09-185-904A-33
Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGGIAAA.....LRGMGGAFVLVLYDELKKVI 298
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 696363 seqs, 186758610 residues
Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum March 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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737	737	749.5	760.5	788.5	811	1385.5	1385.5	1385.5	1454	1454	1454	1543	1543	1543	1 1	Score
47.8	47.8	48.6	49.3	51.1	52.6	89.8	89.8	89.8	94.2	94.2	94.2	100.0	100.0	100.0		Query Match I
308	308	386	318	301	179	297	297	297	298	298	298	298	298	298		Query Match Length DB
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Sequence 8338, Ap	Sequence 3338, Ap	Sequence 170, App	Sequence 252, App	Sequence 7194, Ap	Sequence 32501, A	Sequence 31, Appl		Sequence 31, Appl	Sequence 32, Appl	Sequence 32, Appl	Sequence 32, Appl	Sequence 33, Appl		Sequence 33,	1	Description

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ALIGNMENTS

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MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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OF ADENINE NUCLEOTIDE TRANSLOCATOR LIGANDS AND SCREENING ASSAYS THERE

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TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660086.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORCANISM: Homo sapien
US-09-810-644-33
                                                                                                                                                                                           RESULT 3
US-09-185-904A-33
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APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
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                                                                                                                      Sequence 33, Application US/09185904A Patent No. US20020177185A1
                                                                             GENERAL INFORMATION:
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Best Local Similarity 100.0%; Score 1543;
Best Local Similarity 100.0%; Pred. No. 1e
Matches 298; Conservative 0; Mismatches
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        APPLICANT:
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Anderson, Christen Davis, Robert E.
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Willer, Scott W.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGAND
TITLE OF INVENTION TRANSLOCATOR (ANT), NOVEL ANT LIGAND
TITLE OF INVENTION NUMBER: US/09/185,904A
CURRENT FALING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
TYPE: PRT
; TYPE: PRT
; ORGANISM: Homo
US-09-811-094-32
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US-09-185-904A-33
                                                       NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 32
LENGTH: 298
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                                                                                                                                TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT), TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR FILE REFERENCE: 660088 420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                             APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
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Clevenger, William
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Pred. No. 1e-156;
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Query Match Best Local Similarity

94.2%;

Score Pred.

1454; DB 9; No. 3.5e-147;

Length

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TÎTLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASLEEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo Bapien
US-09-810-644-32
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APPLICANT: Davis, Ro
APPLICANT: Clevenger
APPLICANT: Wiley, Sa
APPLICANT: Willer, S
APPLICANT: Szabo, To
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5. US20020012992A1
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Willer, Scott W.
Szabo, Tomas R.
Ghosh, Soumitra S.
Moos, Walter H.
Pei, Yazhong
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APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiley, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Szabo, Tomas R.
APPLICANT: Moos, Walter H.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT APPLICATION NUMBER: 2001-03-14
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US-09-185-904A-32
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APPLICANT: Anderson;
APPLICANT: Davis, R
APPLICANT: Clevenge
APPLICANT: Wiley, S
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CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/09811094 Patent No. US20010044144A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 274; Conserv
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Patent No. US20020177185A1
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APPLICANT: Willer, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Scot, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND
TITLE OF INVENTION: THEREFOR
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ORGANISM: Homo sapien
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Pred. No. 3.5e-147;
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Indels Length

0;

Gaps

60

296

240

SCREENING

ASSAYS

SOFTWARE: FastSEQ SEQ ID NO 31

for

Windows Version

LENGTH:

297

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; ORGANISM: Homo sapien
US-09-811-094-31
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for SEQ ID NO 31
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APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING
FILE REFERENCE: 660088 420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Wiler, Scott W.
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                        LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
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les 260; Conserv
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GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                        IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
                                                                                                                     MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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Pred. No. 7.5e-140;
21; Mismatches 16; Indels
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Pred. No. 7.5e-140;
11; Mismatches 16;
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SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-31
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                                                                                                           Sequence 32501, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
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APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIC
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
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CURRENT FILING DATE: 1998-11-03
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260; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wiley, Sandra Eileen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.8%; Score 1385.5; DB 10
87.2%; Pred. No. 7.5e-140;
tive 21; Mismatches 16;
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FILE REFERENCE: AEOMICA-X-2

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US-10-032-585-7194
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32501
LENGTH: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7194, Application US/1 Publication No. US20030180953A1
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Terry, Roemer D.
                                                                                                                                                                                                                                                                                                                                    LENGTH: 301
TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 2.00e-83
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OTHER INFORMATION: MAP TO AC004000.1
OTHER INFORMATION: EXPRESSED IN LUNG
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 184
                                                                126 TSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
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52; Conservative
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Bo, Boone
IIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMMQS 242
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                                                                                                                                                                           NFFVDFMMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKQGRLEKRYTGIVDCFKRTAADE 64
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                                 TSLAFVYSLDYARTRLANDAKSSKGDGKREFNGLVDVYKKTLASDGIAGLYRGFGPSVIG
                                                                                                       GVVSFWRGNTANVIRYFPTQALNFAFKDKFKAMF--GFKKDENYWKWFAGNLASGGLAGA
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                                                                                                                                                                                                                                                                 Score 788.5; DB 1
Pred. No. 6.3e-76;
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RESULT 13
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Best Local
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
FRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-20
RIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
NUMBER OF SEQ ID NOS: 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                           260
                                                                                                               243
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                                                                                                                                                                                                                                                         126 TSLCFVYPLDFARTRLAAD--VGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQG 183
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                                                                                                                                                                                                                                                                                             82 GVISFWRGNTANVIRYFPTQALNFAFKDKIKAMF--GFKKEEGYAKWFAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                 66 GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA 125
                                                                                                                                                                                                                                                                                                                                                                    22 NFLIDFLMGGVSAAVAKTAASPIERVKLLIQNQDEMLKQGTLDRKYAGILDCFKRTATQE
                                                                                                                                                                                                                                                                                                                                                                                           7 SFÄKDFLAGGIAAAISKTAVAPIERVKLLLQVQ-HASKQIAADKQYKGIVDCIVRIPKEQ
                                                                                                                                                                               III YRAAY FGVYDTAKG-ML POPKNTHIVVSWMIAQTVTAVAGVVSY PFDTVRRRMMQS
                                                                                                                                                                                                                     LSLLFVYSLDYARTRLAADSKSSKKGGARQFNGLIDVYKKTLKSDGVAGLYRGFLPSVVG 199
                                                                                                         GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
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Salama, Sofie
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No. US20020128250Alman,
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Madden, Kevin
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Silva, Jeff
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Pred. No. 6.8e-73;
Pred. No. 6.8e-73;
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Sequence 170, Application US/09734569 Patent No. US20020064816A1 GENERAL INFORMATION:

APPLICANT: Lerchl,

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FILE REFERENCE: BASF-NAE-1332-99-US
CURRENT APPLICATION NUMBER: US/09/734,569
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/171,101
PRIOR APPLICATION NUMBER: US 60/171,101
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.1/WordPerfect 6.1
SEQ ID NO 170
LENGTH: 386
Type. Tom.
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Best Local
            APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Eroshkin, Alexey M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
CURRENT FILING NUMBER: US/10/128,714
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
RRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
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APPLICANT:
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ITILE OF INVENTION: in the synthesis of carbohydrates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 SGEA---VKYNGSMDAFKQILAKEGAKSLFKGAGANILRAVAGAGVLSGYDQLQ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 GMMSLWRGNTANVIRYFPTQALNFAFKDYFKSLFGYKKDK-DGYWKWFAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157;
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Similarity 53.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIIVYRGLYFGIYDSLKPVVLVGNLEGNFLASFLLGWGITIGAGLASYPIDTVRRRMMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLLFVYSLDYARTRLANDAKSSKKGGGERQFNGLVDVYKKTLATDGIAGLYRGFAISCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFWTDFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMLKSGRLSHPYKGIGECFSRTVKDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duwenig, Elke
Schmidt, Ralf-Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frank, Markus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reindl, Andreas
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NUMBER: US 60/303,899
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Pred. No. 1.3e-71;
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; ORGANISM: Aspergillus US-10-128-714-8338
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                                                                                                                                                         SOFTWARE: PatentIn
SEQ ID NO 8338
LENGTH: 308
Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8338, Application US/10128714
Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3338
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/285,697 PRIOR FILING DATE: 2001-04-23 PRIOR APPLICATION NUMBER: US 60/287,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Exoshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jiang, Bo
APPLICANT: Hu, Wenqi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-04-27 PRIOR APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 TŚGEA---VKYKSSLDAARQIIAKEGVKSLFKGAGANILRGVAGAGVLSIYDQVQLIL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 LGIVVYRGLYFGMYDSIKPVVLVGSLEGSFLASFLLGWTVTTGAGIASYPLDTIRRRMMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 181
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51.7%;
47.8%; Score 737; DB 15; 51.7%; Pred. No. 2.1e-70; rive 47: Mismatches 85;
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Pred. No. 2.1e-70;
                                        Length 308;
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Search completed: Job time : 33 secs	241 244	182 184	124 124	65 4	7
Search completed: December 18, 2003, 17:15:50 Job time : 33 secs	241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298	182 QGIIIYRAAYFGVYDTAKG-MLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM 240 : : : : : : : : : : : :	4 GATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 181	64 EQGYLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGYDKHTQFWRYFAGNLASGGAA 123 - - -	7 SFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK 63

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                 Pred. No. is the number of results predicted by chance to have a
Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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1543
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Copyright (c) 1993 - 2003 Compugen Ltd.
SUMMARIES
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27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	ω	2	44	Result No.
244	244	245	245	245	245	250.5	250.5	250.5	250.5	250.5	250.5	250.5	250.5	250.5	265	280	280	283.5	286	311	311	314	1385.5	1412	1454	1543	Score
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US-09-172-528-2	US-08-937-466-2	US-09-503-579-4	US-09-318-199-4	US-09-172-528-4	US-08-937-466-4	US-08-775-009-33	US-09-547-983-51	US-08-946-719A-51	US-09-210-681-51	US-08-470-868A-51	US-08-807-861A-51	US-08-518-878B-51	US-08-470-868A-56	US-08-518-878B-56	US-09-142-565-2	US-09-160-119-2	US-09-160-119-4	•	US-09-482-273-118	US-09-312-283C-339	-33	US-09-996-243-289	US-09-434-354-47	US-08-961-871-10	US-09-434-354-48	US-09-434-354-49	ID
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244 15.8 308 3 US-09-503-579-2 243.5 15.8 311 2 US-08-93-2 232.5 15.1 320 2 US-08-93-759-2 232.5 15.1 320 2 US-08-93-750-72 232.5 15.1 320 3 US-09-234-613-12 232.5 14.7 303 1 US-08-294-522B-36 226.5 14.7 303 2 US-08-297-861A-37 226.5 14.7 303 2 US-08-470-868A-37 226.5 14.7 303 2 US-08-470-868A-37 226.5 14.7 303 3 US-08-470-863A-37 226.5 14.7 303 3 US-08-946-719A-37 226.5 14.7 303 4 US-09-547-983-37 226.5 13.3 307 2 US-08-807-861A-56 205.5 13.3 307 3 US-08-807-861A-56 205.5 13.3 307 3 US-08-946-719A-56 205.5 13.3 307 4 US-09-547-983-56	45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	
308 320 320 320 320 300 300 300 300 300 300	205.5	205.5	205.5	205.5	211	222	226.5	226.5	226.5	226.5	226.5	226.5	227.5	232.5	232.5	243.5	244	
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3 US-09-503-579-2 2 US-08-775-009-32 2 US-08-775-009-32 2 US-08-93-750C-12 3 US-09-234-613-12 1 US-08-294-522B-36 1 US-08-294-522B-36 1 US-08-294-522B-37 2 US-08-807-861A-37 2 US-09-210-6813-37 3 US-09-210-6813-37 4 US-09-501-558-4 5 PCT-US94-09799-1 2 US-08-807-861A-56 3 US-09-210-681-56 3 US-09-210-681-56 4 US-09-547-983-56	307	307	307	307	306	293	303	303	303	303	303	303	303	320	320	311	308	
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US-08-961-871-10
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US-09-434-354-48
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APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Bileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Velicelebi, Gonul
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Best Local Similarity 92.6
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                Sequence 10, Applio Patent No. 6013858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
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                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                              APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 298
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                               COUNTRY:
                                                                                                                          CITY: Boulder
                                                                                                                                               STREET:
                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                       Application US/08961871
                                                                                                                                            E: Greenlee, Winner and Sullivan,
5370 Manhattan Circle, Suite 201
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Pred. No. 5.2e-156;
Pred. Mismatches 9;
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GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Velicelebi, Gonul
APPLICANT: Davis, Robert E.
APPLICANT: Davis, Robert E.
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                                                          CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 47, Appl: Patent No. 656256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING TITLE OF INVENTION: INVERACTIONS OF MITOCHONDRIAL COMPONENTS, TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERFILE REFERENCE: 660088.433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
ORGANISM: Homo sapien
                        LENGTH: 2
TYPE: PRT
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APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
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LENGTH: 298 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/961,871 FILING DATE: 31-OCT-1997 CLASSIFICATION: 800
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88.6%; Pred. No. 2.9e-151;
ative 19; Mismatches 15;
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RESULT 5
US-09-996-243-289
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            CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
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Best Local
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
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Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J.
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Napier, Mary A.
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    DATE:
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, Margaret Ann
wart, Timothy A.
                                                                                                                                                                                                                                                                                                                                               Zemin
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    1998-02-25
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Pred. No. 2.9
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                                                      R FILING DATE: 1998-06-16
R APPLICATION NUMBER: 60/01
R APPLICATION NUMBER: 60/01
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R FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/088824
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FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088033
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FILING DATE: 1998-06-04
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SEQ ID NO 339
LENGTH: 469
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Best Local Similarity
                                                                                                                                                                                    Matches
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APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated
TITLE OF INVENTION: and Methods For Their
                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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130 FYYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRA 189
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                                                   LWRGNGINVLKIAPESAIKFMAYEQMKR--LVGSDQET---LRIHERLVAGSLAGAIAQS
                                                                                  FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSLC
                                                                                                                     RHLVAGGGAGAVSRTCTAPLDRLKVLMOV-HASR----SNNMCIVGGFTOMIREGGAKS
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                                                                                                                                                                                                    Score 311; DB 3;
Pred. No. 1.7e-26;
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Pred. No. 7.8e-27;
                                                                                                                                                                                    Mismatches 111;
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23

APPLICATION NUMBER: 60/090435

FILING DATE:

CATION NUMBER: 60/090444

1998-06-24

1998-06-24

LING DATE:

APPLICATION NUMBER: 60/090431

1998-06-24

APPLICATION NUMBER: 60/090429

1998-06-24

FILING DATE:

FILING DATE:

APPLICATION NUMBER: 60/090355

1998-06-23

APPLICATION NUMBER: 60/090246

FILING DATE:

FILING DATE:

APPLICATION NUMBER: 60/089952

1998-06-19 1998-06-19

APPLICATION NUMBER: 60/090252

1998-06-22

FILING DATE:

APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

FILING DATE:

FILING DATE:

APPLICATION NUMBER: 60/089801

1998-06-1998-06-17

FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653

NUMBER: 60/089599

1998-06-17

60/089600

1998-06-17

APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19

FILING DATE: APPLICATION NUMBER:

1998-06-18

60/089908

APPLICATION NUMBER: 60/089948

PRIOR PRIOR

FILING DATE: FILING DATE:

APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/090862 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25

1998-06-26 1998-06-26

APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544

FILING DATE: APPLICATION 1

NUMBER: 60/091519

1998-07-01

PRIOR PRIOR PRIOR PRIOR

FILING DATE:

1998-06-25

DR FILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/990678

DR FILING DATE: 1998-06-25

DR PILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090694

DR PILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090694

DR FILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090695

APPLICATION NUMBER: 60/090676

1998-06-24

FILING DATE:

FILING DATE:

APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472

1998-06-24

ING DATE:

1998-06-24

APPLICATION NUMBER: 60/090557

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US-09-482-273-118
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US-09-312-283C-339
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                                                                                                                                                                                                            Sequence 118, Application US/09482273 Patent No. 6534631
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 339
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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ma@ches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/312,283C CURRENT FILING DATE: 1999-05-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
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5. 6573095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 KDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPKEQGVLS 69
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                                                                                                                                                                                                                                                                                                                                             MQAQASIEGAPEVTMSSL--FKQILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK
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Sleeman, Matthew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 311; DB 4;
Pred. No. 1.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 111;
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US-09-501-558-2
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                                                                                                                                                                                         US-09-501-558-2
                                                                                                                                                                                                                                      APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins (
TITLE OF INVENTION: Polynucleotides Encoding the Same FILE REFERENCE: LEX-0012-USA (
CURRENT APPLICATION NUMBER: US/09/501,558 (
CURRENT FILING DATE: 2000-02-09 (
NUMBER OF SEQ ID NOS: 4

SOUTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2
LENGTH: 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                             Query Match
Best Local Similarity
Matches 87; Conserv
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SEQ ID NO 118
LENGTH: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application Patent No. 6403784
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
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QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAG 124
                                                                        KDFLAGGIAAAISKTAVAPIERVKLLLQVQHAS----KQIAADKQYKGIVDCIVRIPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IIYRAAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPPDTVRRRM 238
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                                     KPFVYGGLASITAECGTFPIDLTKTRLQIQGQTNDAKFKEI----RYRGMLHALVRIGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Turner, C. Alexander
Mathur, Brian
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                                                                                                           ; Score 283.5; DB 4;
; Pred. No. 1.1e-23;
54; Mismatches 129;
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Pred. No. 6.9e-24;
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RESULT 11
US-09-160-119-2
; Sequence 2, Application
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US-09-160-119-4
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APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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Best Local .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 447
TYPE: PRT
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                                                                                                                                                                                                 FLRDIPFSAIYFPCYAHVKASFANEDGQVSPGSLLLAGAIAGMPÄASLVTPADVIKTR--
                                                                                                                                                                                                                                                                               GCAGGSQVIFTNPLEIVKIRLQV-AGEITTGPRVSAL----SVVRDLGFFGIYKGAKAC
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US/09160119A

Query Match Best Local Similarity

17.2%; 27.1%;

Score Pred.

265; DB 3; No. 1.5e-21;

Length

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; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO S
US-09-142-565-2
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CURRENT FILING DATE: 1998-09-24

EARLIER APPLICATION NUMBER: EP 97402511.6

EARLIER FILING DATE: 1997-10-23

EARLIER APPLICATION NUMBER: EP 98401655.0

EARLIER FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09142565A
Patent No. 6187569
GENERAL INFORMATION:
APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
APPLICANT: Robert James
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30002
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                                                                                                 NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Best Local Similarity
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                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/142,565A CURRENT FILING DATE: 1999-06-30 EARLIER APPLICATION NUMBER: 9704551.2 EARLIER FILING DATE: 1997-03-05 EARLIER APPLICATION NUMBER: 9705614.7 EARLIER FILING DATE: 1997-03-18 EARLIER FILING DATE: 1997-03-18 EARLIER APPLICATION NUMBER: 97305305.1 EARLIER FILING DATE: 1997-07-16
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APPLICANT: SOUCHET, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: CH-30985
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ORGANISM: HOMO SAPIENS
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                                    Matches
                                                                  Query Match
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                                                                                                                                                                                                            TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                  Local Similarity es 74; Conserv
                                                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                          LENGTH:
                                                                                                                         IOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 QGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTA----VAGVVSYPFDTVRR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GATSLCFVYPLDFARTRLAADV--GKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSV 181
12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
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                                                                                                                                                      1: 299 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGPCSPYNGLVAGLQRQMSFASIRIGLYDSVKQVYTPKGADNSSLTTRILA-----GCTT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATION:
TATTAGIIA, LOUIS A.

TENTION: COMPOSITIONS AND METHODS FOR THE
TOWNTON: TREATMENT OF BODY WEIGHT DISORDERS,
                                                                                                                                                                                                                                              (212) 869-9741/8864
                                    Conservative
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                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-1995
                                16.2%; Score 250.5; DB 1; 24.9%; Pred. No. 6e-20; tive 52; Mismatches 146;
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                                  Indels
                                                                  Length
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US-08-470-868A-56
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APPLICANT: Tartagli
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/470,868A FILING DATE: 06-UM-1995
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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CITY: New York
                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                               ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 --NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56, Application US/08470868A
o. 5861485
    67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                          74;
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SLYNGLVAGLOROMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV 121
                                     SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                   FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68
                                                                              FLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGPR
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                                                                                                                                                                                                                                                                                                                   299 amino acids
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   (212) 869-8864
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ENTION: Compositions and Methods for the
VENTION: Treatment of Body Weight Disorders, Including
                                                                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                                                                                              single
                                                                                                                                                                             16.2%; Score 250.5;
24.9%; Pred. No. 6e
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                                                                                                                                                          Mismatches
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.6e-20;
                                                                                                                                                          Indels 25;
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US-08-518-878B-51
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Best Local S
Matches 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: COTUZZÍ, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE DOCKET NUMBER: 78:
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
US/08/518,878B
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                          y Match 16.2%; Score 250.5; DB 1; Local Similarity 24.9%; Pred. No. 6.3e-20; nes 74; Conservative 52; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 23-AUG-1995 CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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191 CÄELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIÅS----PVDVVKTRYM---
                                       189 AAYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMOS 242
                                                                                    132 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTTAREEGFRGLWKGTSPNVARNAIVN 190
                                                                                                                                129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 -- NSALGQYSSAGHCALIMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 GRKGADIMYTGTVDÇWRKIFRDEGGKAFFKGAMSNVLR-GMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CAELVTYDLIKDALLKANLMTDDLPCHFTSAFGAGFCTTVIAS----PVDVVKTRYM--- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 AAYEGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMMMQS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AVAQPTDVVKVRFQAQ-ARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 CFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYR 188
                                                                                                                                                                                                                                                                   17 FLGAGTAACIADLITFELDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILIMVRTEGPR 76
                                                                                                                                                                             77 SLYNGLVAGLQRQMSFASVRIGLYDSVKQFYTKG-SEHAS----IGSRLLAGSTTGALAV
                                                                                                                                                                                                                         69 SFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSL 128
                                                                                                                                                                                                                                                                                                           12 FLAGGIAAAISKTAVAPIERVKLLLQVQHASK---QIAADKQYKGIVDCIVRIPKEQGVL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 869-9741/8864
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VENTION: COMPOSITIONS AND METHODS FOR THE
VENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
EQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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Qy 243 GRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLR-GMGGAFVLVLYDELKKVI 298
Db 244 --NSALGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 298
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Search completed: December 18, 2003, 17:08:32 Job time: 23 secs

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Title:
Perfect score:
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              1107863 seqs, 158726573 residues
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1454	1454	1454	1463	1543	1543	1543	1543	1543	Score		
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AAU10379	AAU01199	AAY71032	- 1	AAM41427		AAU01200	AAM39641	AAY71033	ij		
adenine	Human adenine nucl	Human adenine nucl	Human insulin rece	Human polypeptide	Human adenine nucl	Human adenine nucl	Human polypeptide	Human adenine nucl	Description		

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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AAG38670	AAG38671	AAG38672	AAG38458	AAG37262	AAG37259	AAG36575	AAG38459	AAG37263	AAG37260	AAG36576	AAG38460	AAG37264	AAG37261	AAG36577	ABP81267	AAM00106	ABG27055	ABG15422	ABP73357	ABG18922	ABP74106	ABP43205	AAE21175	ABU53218	ABB58380	ABB67300	ABB66082	ABG27056	ABG15423	AAU10378	AAU01198	AAY71031	ABU53219 .		ABR41715
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ALIGNMENTS

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RESULT 1
AAY71033
                                  29-AUG-2000
                                                                     AAY71033;
                                                                                                      AAY71033 standard; Protein; 298
Human adenine nucleotide translocator ANT3.
                                (first entry)
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Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.

03-NOV-1998; 08-SEP-1999; 03-NOV-1999; Homo sapiens. 11-MAY-2000 WO200026370-A2 98US-0185904. 99US-0393441. 99WO-US25883.

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AAM39641
ID AAM3
XX AAM3
AC AAM3
XX AAM3
AC AAM3
XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 298; Conserv
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                  AAM39641 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 46; Page 173-174; 175pp; English.
                                                                                                                                                                                                                                  AAM39641
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Ghosh SS;
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                                                                                                                              polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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                                                                                                                                                                                (first entry
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                                                                                                                              SEQ
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                                                                                                                                 ID NO
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                                                                                                                                                                                                                                                                                                    immunosuppresent and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activiny, inhibin activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000; 2000US-0488725
25-APR-2000; 2000US-0552317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-)
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                                                                                                                                                                                                298;
                                                                                                                                                                                                                                                                                               disorders.
                                                                                                                                                                                                                                                                                 The sequence data for this patent
                                                                                                                                                               1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYSEQ INC.
                                                                                                                                                                                                            Similarity
                                                I PKEQGVLS FWRGNLANVI RYF PTQALNFAFKDKYKQI FLGGVDKHTQFWRY FAGNLASG
                                                                                                                                               MTEQAISFAKDFLAGGIAAAISKTAVAFIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                I PKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2786; 10078pp; English.
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; 2000US-0620312.
; 2000US-0653450.
; 2000US-0662191.
; 2000US-0662191.
; 2000US-0693036.
; 2000US-0727344.
                                                                                                                                                                                                Conservative
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Wehrman
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Wehrman T, X
Goodrich R,
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Xu C,
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Pred. No. 4.6e-157;
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                                                                                                                                                                                                                                                                                     CC (ANT-3) protein. ANT proteins are mitochondrial permeability
CC transition (MTP) pore components responsible for mediating transport
CC transition (MTP) pore components responsible for mediating transport
CC falp across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
Cregulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. ANT) fused to an alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalogathy, lactic acidosis, stroke,
                                                                                           Matches
                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitochondrial permeability transition pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                   hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 186pp; English.
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Velicelebi G,
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                                                                                                                   Local
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1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                           Conservative
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                                                                                                                                                                                                                                                                disorders e.g. cancer, and deafness.
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comprising a regulated promoter operably linked to a nucleic acid concoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial contrix for ADP in the cytosol. (I) is useful for producing recombinant NT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is capressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide. ANT cuseful for identifying an agent that binds to an ANT polypeptide. ANT cuseful for determining the presence of an ANT polypeptide. CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating CC ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson (Ghosh SS,
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, Moos WH, Pei Y, Carroll AK;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
14-SEP-2000;
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Wang
Zhao
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                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM41427;
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DB; AAI60583.
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                                                                                                                                                                                                                                                                                                              HYSEQ INC
                                                                                                                                                                                  Liu C,
Wang Z,
Zhou P,
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2000US-0552317.

2000US-0598042.

2000US-0620312.

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                                                                                                                                                                                     Asundi V,
Wehrman T,
Goodrich 1
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                                                                                                                                                                                                           Chen R,
Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323
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Pred. No. 4.6e-157;
Mismatches 0;
                                                                                                                                                                                     len R, Ma
lu C, Xue
Drmanac R
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r; central nervous system; CNS;
                                                                                                                                                                                        a Y,
e AJ,
RT;
                                                                                                                                                                                                                  Qian ;
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                                                                                                                                                                                                                                              Wang
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12-JAN-2001; 2001US-261226P.
12-JAN-2001; 2001US-261303P.
12-JAN-2001; 2001US-261304P.
12-JAN-2001; 2001US-261335P.
12-JAN-2001; 2001US-261336P.
                                                                                                                                                     11-JAN-2002; 2002WO-US01048
                                                                                                                                                                                                         18-JUL-2002
                                                                                                                                                                                                                                                         WO200255664-A2
                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human insulin receptor signaling modifier SEQ ID NO:
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Note: The sequence specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSGRKGADIMYTGTVDCWRK1FRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
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metabolic syndrome;
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Pred. No. 5.2e-157;
Mismatches 0;
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12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent-biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ism function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying an insulin receptor signaling modulator, useful as drug targets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent
                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 160-161; 232pp;
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12-JAN-2001;
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12-JAN-2001;
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                                                                                                                                                                                                                                                                                                              Local
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241
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             QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKK 296
                                                                        VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                                                                             I PKEQGVLSFWRGNLANV I RYF PTQALNF AF KDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                GAAGATSLCFVYPLDFARTRLAADVGKAGAEREFRGLGDCLVKIYKSDGIKGLYQGFNVS
                                                                                                                                                                            IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASG
                                                                                                                                                                                                                                    MTDAAVSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR
                                                                                                                                                                                                                                                      MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKJLLQVQHASKQIAADKQYKGIVDCIVR
                                                         VQGIIIYRAAYFGIYDTAKGMLPDPKNTHIVISWMIAQTVTAVAGLTSYPFDTVRRRMM
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2001US-261531P.
2001US-261532P.
2001US-261532P.
2001US-261549P.
2001US-261694P.
2001US-261694P.
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2001US-261456P.

2001US-261458P.

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; 2001US-261461P.
                                                                                                                                                                                                                                                                                              Conservative
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92.9%;
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                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                             Score 1463; DB 23;
Pred. No. 1.8e-148;
3; Mismatches 8;
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RESULT 7
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AAY71032 standard; Protein; 298

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IPKEQGVLSFWRGNLANVIRYEPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG MTDAALSFAKDFLAGGVAAAISKTAVAPIERVKLLLQVQHASKQITADKQYKGIIDCVVR MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR Matches

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Query Match
Best Local
                                                                                                             as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT2 from human brain.
                                                                                                                                                                                                                                                                                                                                                 The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia, diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidossis; stroke; MIDD; mitochondrial diabetes and deafness; hyperprosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperprosis; stroke; MIDD; myoclonic epilepsy red ragged fibre syndrome.
                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 45; Page 172-173; 175pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD00520.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson CM,
Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1998;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adenine nucleotide translocator; ANT2;
                      Similarity
                                                                             298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide translocator ANT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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99US-0393441.
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                  94.2%;
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Score 1454; D
Pred. No. 1.7e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wiley SE,
                ; DB 21;
l.7e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller SW,
                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Szabo TR;
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                               (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MFT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
                                                                                                                                                                                                                                                                                                  The present sequence represents human adenine nucleotide translocator-2 (ANT-2) protein. ANT proteins are mitochondrial permeability transition (MTP) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin; mitochondrial permeability transition pore component; cell surviva mitochondrial core component; mitochondrial related disorder; canc Anzheimer's disease; diabetes mellitus; hyperproliferative disorde Anzheimer's disease; diabetes mellitus; hyperproliferative disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy AN,
Velicelebi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clevenger W,
3, Davis RE;
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      stroke
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RESULT 9
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Best Local S
Matches 274
The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nuclectide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or enkaryotic host cell a culturing the host cell. (I) is also useful for targețing a polypeptide
                                                                                                                                                                                                                                                              Novel recombinant expression construct for producing adenine nucleotide translocator polypeptides, comprises a regulated promoter linked to nucleic acid encoding the polypeptide •
                                                                                                                                                                                                                  Claim
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)B; AAS16689.
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                                                                                                                                                                                                             44; Fig 2; 147pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOKOR.
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74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CM, Davis
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Pred. No. 1
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Best Local :
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28-MAR-2001;
29-MAR-2001;
29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT2.
                                                                                                                                                                                                                                                                                                                   cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic neurological disorder; gastrointestinal disorder; transport Air
                                                                                                                                     27-MAR-2002;
                                                                                                                                                                    05-DEC-2002
                                                                                                                                                                                                  WO200297031-A2
                                                                                                                                                                                                                                                             organelle-associated
                                                                                                                                                                                                                                                                          neurological disorder; gastrointestinal disorder; transport disorder; commective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in; disease model; toxicological testing; transcript imaging;
                                                                                                                                                                                                                                                                                                                                                                 Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSMMIAQTVTAVAGVVSYPFDTVRRRMM
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              2001US-279619P
2001US-280067P
2001US-280068P
2001US-291280P
2001US-291280P
2001US-291849P
2001US-291849P
2001US-299428P
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                                                                                                                                       2002WO-US10056
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                      The invention relates to novel human diagnostic and therapeutic CC polynucleotides designated dithp (ACC46080-ACC46749) and to their CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA CC transgenic organisms comprising a dithp nucleic acid sequences; methods of creembinant production of DITHP proteins; antibodies specific for DITHP compounds using a dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein; and methods of compounds which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein; and methods of compounds which specifically bind a DITHP protein; and methods of conditions including cancer and other cell probe. Dithp nucleic acid sequences and DITHP proteins may be used in the conditions including cancer and other cell conditions; normanal disorders; metabolic conditions; normanal disorders; bacterial, curial, fungal or parasitic infections; hormonal disorders; transport consorders; and connective tissue disorders; They may also be used to coroll type and to induce antibodies. The dith nucleic acids are cadditionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of protein antibodies. The dith nucleic acids are cadditionals, in toxicological testing, and in transcript imaging. The present sequence represents a DITHP protein which is an organelle-
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                 Query Match
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Dufour GB, Hillman ...,
Daughtery SC, Dam TC,
Peralta CH, David MH,
Plant CH, Marwaha R, J
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to
                                                                                                                                                                                                                                                                                                                                                                                          specification,
                                                                                                                                                                                                                                                                                                                                                                                                                          associated protein.
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                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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DB; ACC46652.
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                                                                     GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                                                                                                        MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
                                                                                                                                        I PKEQGVLS FWRGNLANVIRYF PTQALNFAFKDKYKQI FLGGVDKHTQFWRYFAGNLASG
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                                                                                                                     I PKEQGVLS FWRGNLANVIRY FPTQALNFA FKDKYKQI FLGGVDKHTQ FWRY FAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                        sequence data for this patent did no tion, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ
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                                                                                                                                                                                                                                                               Conservative
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TC, Liu TF, Nguyen
                                                                                                                                                                                                                                                                                91.9%;
95.2%;
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Pred. No. 2
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Lan RY,
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Kleefeld
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Harris B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the mouse Antl protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Antl cDNA as a probe. The Antl cDNA sequence was determined by DNA Taq dideoxy terminator cycle sequencing. The Antl protein is encoded by the Antl locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Antl homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Antl homozygous mutant can be used as a model system for fascioscapular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of ATP and ADP exchange across the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mice lacking heart-muscle adenine nucleotide translocator protein useful as model for mitochondrial myopathy and hypertrophic cardiomyopathy in animals and to test therapeutic compositions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graham BC,
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 39-40; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW61169 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEM-) UNIV EMORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ant1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 -OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gp.
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   61
                                                         61
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV36479
                                   I PKEQGVLS FWRGNLANVI RYF PTQALNFA FKDKYKQI FLGGVDKHTQFWRYFAGNLASG
                                                                                                                     MGDQALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
                                                                                                                                                            MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
   I PKEQGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGA-W----SNVLRGMGGA
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                                                                                                                                                                                                                                                                                                                                                                           298
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                                                                                                                                                                                                                                                                                                                                                                                                                                    of ANT1.
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                           91.5%;
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                                                                                                                                                                                                                                                  19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298
                                                                                                                                                                                                                                               Score 1412; DB 19;
Pred. No. 5.4e-143;
.9; Mismatches 15;
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ALSFLKDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKE

Best Loc Matches Query Match

263;

Conservative

17;

Mismatches

Indels Length

Gaps

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293; 0,

Local

Similarity

91.1%; 90.1%;

Score 1406; Pred. No. 2

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                            from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention.
 Sequence
                                                                                                                                                                                                                              Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in {\it recombinant DNA methodologies} -
                                                                                                                                                                                                                                                                              WPI; 2001-327840/34
                                                                                                                                                                                                                                                                                                                                                                       18-AUG-1999;
28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human metabolism-associated DKFZphtes3_35n12 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU53219
                                                                                                                                                                  This invention describes novel polynucleotides and polypeptides isolated
                                                                                                                                                                                                  Example III; Page 850; 1095pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-2000; 2000WO-IB01496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200112659-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU53219;
                                                                                                                                                                                                                                                                                                                                          (GEHU-) GERMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGATSLCFVYPLDFARTTLAADVGKGSSQREFNGLGDCLTKIFKSDGLKGLYQGFSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSGRKGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQGIIIYRAAYFGVYDTAKGMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMM
   293
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   AA,
                                                                                                                                                                                                                                                                                                                                          HUMAN GENOME PROJECT
                                                                                                                                                                                                                                                                                                                                                                     99US-0149499
99US-0156503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease treatment; detection
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ARESULT 13
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The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzhelmer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ghosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant construct encoding adenine polypeptide, useful e.g. in screening against mitochondrial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-365619/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson CM,
Ghosh SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adenine nucleotide translocator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGADIMYTGTLDCWRKIAKDEGANAFFKGAWSNVLRGMGGAFVLVLYDEIKK 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0185904.
99US-0393441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide translocator for potential therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiley SE,
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RESULT 14
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Best Local
                                                                                                                                            New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
                                                                                                                                                                                                                                                                                                                                                                         Murphy AN, C:
Velicelebi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitochondrial mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an adenine nucleotide translocator ANT1 from human brain.
                                                                                                                                                                                                                                                                                                                   WPI; 2001-291054/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-NOV-2000; 2000WO-US30535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin; ondrial permeability transition pore component; cell surviva ondrial core component; mitochondrial related disorder; canc mer's disease; diabetes mellitus; hyperproliferative disorde
                                                                                                                                                                                                                                                                                           AAS05901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGDHAWSFLKDFLAGAVAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVR
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                                                                                                                                                                                                                                                                                                                                                                                                    Clevenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide translocator-1 (ANT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0434354
                                                                                                                                                                                                                                                                                                                                                                            RE;
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Pred. No. 3.8e-140;
                                                                                                                                                                                                                                                                                                                                                                                                    SE,
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                                                                                                                                                                                                                                                                                                                                                                                                       Andreyev
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                                                                                                                                                                                                                                                                                                                                                                                                       ΑY,
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                                                                                                                                                                                                                                                                                                                                                                                                       Frigeri LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   survival;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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The present sequence (ANT-1) protein. ANT

represents human adenine nucleotide translocator-1 proteins are mitochondrial permeability

Disclosure;

Fig

2; 186pp; English

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RESULT 15
AAU10378
ID AAU10
XX AAU10
XX AAU10
XX 14-FE
DT 14-FE
DZ Human
XX Mitoc
CX Mitoc
CX MO200
XX MO200
XX Homo
XX MITC
XX MITC
XX MITC
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PI Ander
PI Ander
PI Ander
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression construct can alter mitochondrial membrane permeability transition and/or alter the interaction between mitochondrial core components. The methods are useful for screening for agents that alter MPT and/or cell survival. These agents are useful for the prevention or treatment of diseases associated with altered mitochondrial function or dysfunctional cell survival, such as Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis, stroke, hyperproliferative disorders e.g. cancer, and deafness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability
                        Anderson CM, Davis RE,
Ghosh SS, Moos WH, Pei
                                                                                                                                                                                                                                                                                        WO200185944-A2
                                                                                                                                                                                                                                                                                                                                                                                   Human; adenine nucleotide translocator; ANT; mitochondrial matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                            11-MAY-2000; 2000US-0569327
                                                                                                                                                                                           11-MAY-2001; 2001WO-US15416
                                                                                                                                                                                                                                            15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                  (MITO-) MITOKOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenine nucleotide translocator 1 (ANT1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
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Y, Carroll AK;
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                                                 Wiley SE,
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                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant expression construct (I) CC comprising a regulated promoter operably linked to a nucleic acid cencoding an adenine nucleotide translocator (ANT) polypeptide. ANT contributed by transforming a prokaryotic host cell and culturing the host cell. (I) is useful for producing recombinant CC matrix for ANP in the cytosol. (I) is useful for producing recombinant CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and CC culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is CC expressed as a fusion protein with the polypeptide of interest. CC useful for identifying an agent that binds to an ANT polypeptide. ANT CC ligand is useful for determining the presence of an ANT polypeptide. CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating CC ant from a biological sample, where the ANT ligand is covalently or non-CC covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT1.
                                                                                                                                                                                                                                                                   Query Match
Best Local (
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  GAAGATSLCFVYPLDFARTRLAADVGRR-AQREFHGLGDCIIKIFKSDGLRGLYQGFNVS
                         GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVS
                                                                                                            IPKEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASG
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Search completed: December 18, 2003, 17:10:50 Job time : 43 secs

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QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMGGAFVLVLYDELKKVI 298

ÓSGRKGADIMYTGTVDCWRKIAKDEGAKAFFKGAWSNVLRGMGGAFVLVLYDEIKKYV 297

VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMM

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"Two distinct genes for ADP/ATP translocase are expressed at t	DF 36-298 FROM /er; 3124845; PubMed	Proc. Natl. Acad. Sci. U.S.A. 9	"Generation and initial analysis of more than 15,000 full-	Butterfield V.S.N., Krzywinski M.I., Skaliska U Schnerch A. Schoin J.R. Jones S.J.M. Marra M	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., S Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gun Richards S. Worley K.C. Hale S. Garcia A.M. Gav L.J	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D.,	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Ho Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L.,	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler	TISSUB-BIAIN, CEIVIX, Bye, and Lung; MEDLINE-22388257; PubMed=12477932; Charline-2388257; Primorla P. 7 932;	SEQUENCE FROM N.A.	Submitted (JU	Zhou J., Yu	[2]	ADP/ATP transfer of Captions and the ADP/ATP transfer of Captions	MEDLINE=89236396; PubMed=2541251; COZENS AL., Runswick M.J., Walker J.E.; Thus esquares of two expressed nuclear genes for	Α.	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Hom NCBI_TaxID=9606;	Guerrota: Metagoa: Chordata: Cramiata: Vortebrata: Ente Enternota: Metagoa: Chordata: Cramiata: Vortebrata: Ente	(Adenine nucleotide translocator 3) (ANT 3).	15-SEP-2003 (Red. 42, Last ann ADP.ATP carrier protein. liver	01-OCT-1989 (Rel. 12, Created)	T3_HUMAN ADT3_HUMAN	DECIT T	ALIGNMENTS	4 265 17.2 312 1 UCP3_HUMAN P55916 5 265 17.2 676 1 CMC2_MOUSE Q9qxx4	270 17.5 315 1 SAIR HUMAN O9hlkd	0 282.5 18.3 326 1 YEON SCHPO 013805	8 285 18.5 332 1 GDC HUMAN P16260 9 284 18.4 325 1 UCP5 MOUSE Q9z2b2	6 287.5 18.6 702 1 CMCT_CAEEL Q21153 7 286 18.5 325 1 UCPS_HUMAN 095258
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PRINTS; PRO0784; MITUNCOUPLING.
PRO0215; MITOCH CARRIER; 3.
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InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
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GO:0005744; C:mitochondrial inner membrane
GO; GO:0005471; F:ATP/ADP antiporter activity;
GO; GO:0006854; P:ATP/ADP exchange; TAS.
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Genew; HGNC:10992; SLC25A6.
MIM; 300151; -.
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SUBCELLULAR LOCATION: Integral
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L; BC008935; AAH08935.1; -.

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tl. Acad. Sci. U.S.A. 85:377-381(1988).
TION: CATALYZES THE EXCHANGE OF ADD AND ATP ACROSS
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Pred. No. 3.6e-128;
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F (IN REF. 3; AAH14775).
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                                                                                         SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=89229093; PubMed=2540808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda Bovidae; Bovinae; Bos.
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16-OCT-2001
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InterPro; IPR002030; Mit_
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                                                                                                                                                                                                                              Multigene family.
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SIMILARITY: Belongs to the mitochondrial carrier family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane.
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                                                                                                                                                                                                                                                                                                        IPR002067; Mit_carrier.
IPR002030; Mit_uncoupling.
IPR001993; Mitoch_carrier.
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                                                                                          298 AA;
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                                       Conservative
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                                     Score 1512; DB 1;
Pred. No. 1.9e-125;
4; Mismatches 3;
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241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGWGGAFVLVLYDELKKVI 298

ÓŚGRKGADIŃYKOTVDCWRKILKDEGGKAFFKGAWŚNVLRGMGGAFVLVLYDELKKVI

181 VQGIIIYRAAYFGVYDTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPEDTVRRRMMM 240

VÓGÍ Í Í ÝRÁAÝ FGTÝÐTÁKGMÍ ÞÐ ÞKNTHÍ VVSMNÍ ÁÐ TVTÁVÁG VVSÝ ÞEÐ TVRRRMAN

GAAGATSLCPVYPLDFARTRLAADVGKSGSEREFRGLGDCLVKITKSDGIRGLYQGFNVS

180 180 120 120

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Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
-I- SUBUNIT: Homodimer.

    -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
    -!- SIMILARITY: Belongs to the mitochondrial carrier family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE:
SEQUENCE:
TISSUE=Blacenta;
MEDLINE=90375457; PubMed=2168878;
MED.-H., Kagan J., Chen S.-T., Chang C.-D.,
"The human fibroblast adenine nucleotide trar
cloning and sequence.";
"Riol. Chem. 265:16060-16063(1990)
                                                                                                                                                                                                   SEQUENCE OF 47-298 FROM N.A.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Becker M., Graves T., Ozersky P.,
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,

Mazzarella R.A., Schlessinger D., Chen E.Y.;

Submitted (JUN-1996) to the EMBL/GenBank/DDBU databases.
                                                                                                                                                                      MEDLINE=88124845; PubMed=2829183;
                                                                                                                                                                                             TISSUB=Liver;
                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of a cDNA for a human ADP/ATP carrier which growth-regulated.";
                                                                                                                                                                                                                                                                                                                                                                                                       Battini R., Ferrari S., Kaczmarek L., Calabretta B.,
Baserga R.,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase
(Adenine nucleotide translocator 2) (ANT 2).
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                                          SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
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ADT2_RAT STANDARD; Q09073; Q1-FEB-1995 (Rel. 31, Created)

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PRINTS; PR00926; MITOCARRIER.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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InterPro; IPR002030; Mit uncoupling.
InterPro; IPR001993; Mitoch carrier.
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EMBL; J02683; AAA35579.1; --
EMBL; L78810; AAB39266.1; --
EMBL; AC004000; AAB96347.1; --
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                               ÓSGRKGTDÍMÝTGTLDCWRKÍARDEGGKAFFKGÁWSNVLRGMGGÁFVLVLÝDEIKK
                                           QSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGWGGAFVLVLYDELKK 296
                                                                                   GAAGATŠLĆĖVYĖLDĖARTRLAADVGKAGAEREFRGLGDČLVKI YKŠDGI KGLYQGENVS
                                                                       VQGIIIYRAAYEGIYDTAKGMLEDEKNTHIVISMMIAQTVTAVAGLTSYPEDTVRRRMMM
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Pred. No. 3.8e-121;
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                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
(POTENTIAL)
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                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                        NI)
NI)
                                                                                                                                                                                                                                                                                                       REF.
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5).
                                                                                                                                                                                                                                                                    Length 298;
                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                              Gaps
                               296
                                                                                           240
                                                                                                                 180
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